

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
944	1hle	A	175	498	7e-99			132.76	HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
944	1i99	I	168	532	1.5e-64			167.27	ALASERPIN; CHAIN: I; TRYPSIN II, ANIONIC; CHAIN: E; 3	HYDROLASE/HYDROLASE INHIBITOR SERPIN 1; PRETRYPSINOGEN II; MICHAELIS SERPIN-PROTEASE COMPLEX INHIBITORY TRIAD
944	1i99	I	6	370	7e-81			169.22	ALASERPIN; CHAIN: I; TRYPSIN II, ANIONIC; CHAIN: E;	HYDROLASE/HYDROLASE INHIBITOR SERPIN 1; PRETRYPSINOGEN II; MICHAELIS SERPIN-PROTEASE COMPLEX INHIBITORY TRIAD
944	1ova	A	12	370	2.8e-94			151.89	SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
944	1ova	A	174	532	1.4e-96			151.52	SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
944	1ova	A	176	532	1.4e-96	0.53	1.00		SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
944	1qlp	A	12	372	0			171.59	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR-ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE

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944	1q1p	A	174	534	0			170.59	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
944	1q1p	A	175	532	0	0.46	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
944	1q1b	B	502	532	9.8e-09	-0.75	0.05		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-PI; SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
944	1q1m	A	14	372	0			184.90	ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
944	1q1m	A	176	533	0	0.46	1.00		ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION,

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944	1qmn	A	176	534	0			183.22	ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
944	1sek		168	532	1.4e-81			143.79	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
944	1sek		6	370	2.8e-80			145.58	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
945	1f3l	A	80	188	4.2e-25	0.40	1.00		PROTEIN ARGININE METHYLTRANSFERASE PRMT3; CHAIN: A;	TRANSFERASE BETA BARREL, ROSSMANN FOLD, ARGININE METHYLTRANSFERASE
945	1f3l	A	80	213	1.7e-05	-0.30	0.23		PROTEIN ARGININE METHYLTRANSFERASE PRMT3; CHAIN: A;	TRANSFERASE BETA BARREL, ROSSMANN FOLD, ARGININE METHYLTRANSFERASE
945	1g6q	1	81	219	1.4e-25	0.03	0.57		HNRP ARGININE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
947	1av1	A	1	193	2.8e-09			56.50	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
947	1c1g	A	13	296	1.3e-29			96.22	TROPOMYOSIN; CHAIN:	CONTRACTILE PROTEIN

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									A, B, C, D	TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
947	1clg	A	249	532	4.2e-28			105.38	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
947	1cun	A	190	417	1.7e-13	0.09	-0.05		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1cun	A	249	504	3.4e-19	0.11	0.52		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1cun	A	412	536	6.8e-08	0.05	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1cun	A	4	206	0.0097			56.15	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1cun	A	55	271	0.00011			69.05	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
947	1dn1	B	1	190	0.0025			55.90	SYNTAXIN BINDING PROTEIN 1; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN

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									SYNTAXIN 1A; CHAIN: B;	COMPLEX, MULTI-SUBUNIT
947	1dn1	B	366	527	1.2e-12	0.13	-0.15		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
947	1dn1	B	53	284	0.0066			63.83	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
947	1dvp	A	475	575	3.4e-20	-0.06	0.28		HEPATOCYTE GROWTH FACTOR-REGULATED TYROSINE CHAIN: A; SSO1 PROTEIN; CHAIN: A;	TRANSPERASE HRS; HRS, VHS, FYVE, ZINC FINGER, SUPERHELIX
947	1fio	A	2	191	0.0097			62.09	SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
947	1hci	A	126	570	1.7e-30			114.13	ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE 2 Z-LINE, ACTIN-BINDING PROTEIN
947	1hci	A	188	553	1.7e-29	-0.13	0.22		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE 2 Z-LINE, ACTIN-BINDING PROTEIN
947	1hci	A	189	511	1.7e-30	-0.15	0.10		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN,

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										MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
947	1byi	A	531	580	5.1e-19	0.11	0.75		ENDOSOME-ASSOCIATED PROTEIN; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SHEET, ALPHA HELIX, ZINC CLUSTER, PTDINS(3)P
947	1byi	A	5	68	1.1e-19			62.30	ENDOSOME-ASSOCIATED PROTEIN; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SHEET, ALPHA HELIX, ZINC CLUSTER, PTDINS(3)P
947	1quu	A	297	517	1.7e-18	0.11	-0.15		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
947	1vfy	A	531	575	6.8e-16	-0.08	0.69		PHOSPHATIDYLINOSITOL-3-PHOSPHATE BINDING FYVE CHAIN: A;	TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN
947	1zbd	B	496	603	6.8e-23	0.02	-0.02		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
950	1b6e		111	237	5.6e-26			94.09	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
950	1b6e		1	118	7e-25			76.63	CD94; CHAIN: NULL;	NK CELL NK CELL, RECEPTOR, C-TYPE LECTIN, C-TYPE LECTIN-LIKE, NKD
950	1bj3	A	112	233	2.8e-36	0.21	0.69		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A;	COLLAGEN BINDING PROTEIN IX-BP, IX-BP, COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2

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									IX-BINDING PROTEIN B; CHAIN: B;	SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
950	1bj3	A	112	234	2.8e-36			66.57	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
950	1c3a	B	110	236	1.4e-35			68.42	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
950	1c3a	B	112	236	1.4e-35	0.48	1.00		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
950	1c3a	B	1	117	1.3e-30			50.64	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
950	1dv8	A	113	233	1.4e-32	0.63	1.00		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A; ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
950	1dv8	A	113	241	1.4e-32			69.21	ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
950	1e87	A	111	236	5.6e-27			81.55	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR
950	1e87	A	1	117	1.1e-24			60.58	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	HEMATOPOIETIC CELL RECEPTOR ACTIVATION

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									A;	INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR
950	1egg	A	113	236	4.2e-28			53.59	MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
950	1egg	B	110	241	7e-29			60.69	MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
950	1fyu	A	112	237	4.2e-30			52.01	BOTROCETIN ALPHA CHAIN: CHAIN: A, C; BOTROCETIN BETA CHAIN: CHAIN: B, D;	TOXIN PLATELET COAGGLUTININ ALPHA; PLATELET COAGGLUTININ BETA VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1fyu	B	112	236	4.2e-34	0.58	0.99		BOTROCETIN ALPHA CHAIN: CHAIN: A, C; BOTROCETIN BETA CHAIN: CHAIN: B, D;	TOXIN PLATELET COAGGLUTININ ALPHA; PLATELET COAGGLUTININ BETA VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1fyu	B	112	236	4.2e-34			69.59	BOTROCETIN ALPHA CHAIN: CHAIN: A, C; BOTROCETIN BETA CHAIN: CHAIN: B, D;	TOXIN PLATELET COAGGLUTININ ALPHA; PLATELET COAGGLUTININ BETA VON WILLEBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1fyu	B	1	117	1.4e-28			50.65	BOTROCETIN ALPHA CHAIN: CHAIN: A, C; BOTROCETIN BETA CHAIN: CHAIN: B, D;	TOXIN PLATELET COAGGLUTININ ALPHA; PLATELET COAGGLUTININ BETA VON WILLEBRAND FACTOR

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										MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
950	1hq8	A	108	237	4.2e-30			93.99	NKG2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
950	1hq8	A	1	118	2.8e-28			66.38	NKG2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
950	1hyr	A	107	237	4.2e-28			92.55	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE-LECTIN LIKE, MIC-2 A, MHC-I, COMPLEX, IMMUNE SYSTEM
950	1hyr	A	1	118	5.6e-24			65.31	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE-LECTIN LIKE, MIC-2 A, MHC-I, COMPLEX, IMMUNE SYSTEM
950	1iod	A	112	233	1.3e-33	0.13	0.82		COAGULATION FACTOR X BINDING PROTEIN; CHAIN: A; COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
950	1iod	A	112	234	1.3e-33			59.17	COAGULATION FACTOR X BINDING PROTEIN; CHAIN: A; COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING

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950	liod	B	112	236	9.8e-36	0.56	1.00		X GLA DOMAIN; CHAIN: G ₁ COAGULATION FACTOR X BINDING PROTEIN; CHAIN: A; COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G ₁	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
950	liod	B	112	236	9.8e-36			60.25	COAGULATION FACTOR X BINDING PROTEIN; CHAIN: A; COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G ₁	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
950	lixx	A	112	233	7e-34	0.19	0.76		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G ₁	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	lixx	A	112	234	7e-34			62.61	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G ₁	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	lixx	B	112	236	9.8e-36	0.48	1.00		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G ₁	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER

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									C, D, E, F;	DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	1ixx	B	112	236	9.8e-36			65.36	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
950	1lit		113	235	4.2e-35	0.65	1.00		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
950	1lit		113	241	4.2e-35			59.42	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
950	1lit		1	122	1.3e-28			52.81	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR, LECTIN
950	1qdd	A	101	235	9.8e-36	0.52	1.00		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
950	1qdd	A	101	241	9.8e-36			64.36	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
950	1qo3	C	105	236	6.8e-27			72.18	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YB1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M,

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950	1qo3	C	1	117	4.2e-25			52.76	LY49A; CHAIN: C, D; MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	LY49, LY-49 COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
950	1qo3	D	115	238	7e-26			65.45	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
950	1qo3	D	1	119	4.2e-25			56.68	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
950	1tm3		108	238	2.8e-28			50.25	TETRANECTIN; CHAIN: NULL;	LECTIN TETRANECTIN, PLASMINOGEN BINDING, KRINGLE 4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
950	2afp	A	107	241	2.8e-29			63.07	SEA RAVEN TYPE II ANTIFREEZE PROTEIN;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A;	PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
951	1bj3	A	198	280	4.2e-26	0.10	0.09		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
									FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
951	1c3a	B	197	281	4.2e-27	0.10	0.39		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	SIGNALING PROTEIN HEPATIC LECTIN H; C-TYPE LECTIN CRD
951	1dv8	A	198	276	1.4e-24	0.22	0.68		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A; BOTROCETIN ALPHA CHAIN; CHAIN: A, C; BOTROCETIN BETA CHAIN; CHAIN: B, D;	TOXIN PLATELET COAGULUTININ ALPHA; PLATELET COAGULUTININ BETA VON WILBRAND FACTOR MODULATOR, C-TYPE LECTIN, METAL-2 BINDING, LOOP EXCHANGED DIMER
951	1fva	B	198	280	1.4e-26	0.07	0.47			
									NKG2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
951	1hq8	A	193	280	8.4e-28	0.17	0.58		NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE LECTIN LIKE, MIC-2 A, MHC-I, COMPLEX, IMMUNE SYSTEM
951	1hvr	A	192	279	1.4e-25	-0.08	0.90		COAGULATION FACTOR X BINDING PROTEIN; CHAIN: A;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
951	1iod	A	198	280	7e-25	0.02	0.19			

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
951	1iod	B	198	280	2.8e-25	-0.02	0.01		COAGULATION FACTOR X BINDING PROTEIN; CHAIN: B; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G;	HYDROLASE/HYDROLASE INHIBITOR CALCIUM BRIDGING, DOMAIN SWAPPING
951	1ixx	B	198	281	4.2e-26	-0.12	0.09		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; COAGULATION FACTOR X GLA DOMAIN; CHAIN: G;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
951	2afp	A	193	281	1.4e-24	0.38	0.46		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
952	1g9r	A	1242	1507	1e-44	0.19	0.93		GLYCOSYL TRANSFERASE; CHAIN: A;	TRANSFERASE ALPHA-BETA STRUCTURE
953	1a17		68	229	2.8e-16	0.33	1.00		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP, HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
953	1elr	A	152	227	0.00014	0.14	0.60		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
953	1elr	A	65	218	1e-09	0.22	0.99		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
953	1elw	A	65	217	1.7e-13	0.47	0.81		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
953	1elw	A	68	215	1.3e-08	0.44	0.95		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
953	1feh	A	71	226	3.4e-09	0.20	0.62		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
953	1hh8	A	150	198	2.8e-05	0.06	0.43		NEUTROPHIL CYTOSOL FACTOR 2; CHAIN: A;	PHAGOCYTE OXIDASE FACTOR P67PHOX, NCF-2; PHAGOCYTE OXIDASE FACTOR, SH3 DOMAIN, REPEAT, TPR REPEAT
953	1ihg	A	68	226	8.4e-37	0.39	1.00		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPLASE IMMUNOPHILIN TETRATRICOPEPTIDE
957	1fnf		1	203	5.6e-32	-0.35	0.18		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
957	1fnh	A	1	192	1.3e-27	-0.20	0.11		FIBRONECTIN; CHAIN:	HEPARIN AND INTEGRIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A;	BINDING HEPARIN AND INTEGRIN BINDING
957	1fhh	A	31	201	2.8e-22	-0.22	0.27		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
957	1i1r	A	29	202	1.3e-12	0.14	-0.19		INTERLEUKIN-6 RECEPTOR BETA CHAIN; CHAIN: A; VIRAL IL-6; CHAIN: B;	CYTOKINE GP130; FUNCTIONAL INTERLEUKIN-6 HOMOLOG; CYTOKINE/RECEPTOR COMPLEX, GP130, VIRAL IL-6, CRYSTAL 2 STRUCTURE
957	1mfn		29	204	4.2e-29			66.80	FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
957	1mfn		2	112	1.4e-23	0.12	-0.08		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
957	1mfn		31	203	4.2e-29	0.11	0.41		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
957	1qg3	A	29	194	4.2e-24			57.81	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
957	1qr4	A	31	204	2.8e-21			71.24	TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
957	1qt4	A	33	193	2.8e-21	0.01	0.27		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
957	1qt4	A	3	117	7e-20	-0.25	0.84		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
957	1ten		11	98	8.4e-16			53.41	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	
957	1ten		30	117	1.7e-18			53.70	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	
957	1ttf		11	99	4.2e-21			51.26	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	
957	1ttf		30	121	8.4e-18			51.78	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	
958	1cge		123	282	5.6e-71	1.17	1.00		HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I 1CGE 3	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
958	1cge		123	283	5.1e-74			280.54	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I 1CGE 3	
958	1cge		123	284	5.1e-74	1.12	1.00		HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I 1CGE 3	
958	1cge		76	188	4.2e-55			176.37	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I 1CGE 3	
958	1ck7	A	27	246	4.2e-73	0.27	0.99		GELATINASE A; CHAIN: A; 3	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL- LENGTH, METALLOPROTEINASE, 2 GELATINASE A
958	1fb1		121	487	0	1.03	1.00		FIBROBLAST (INTERSTITIAL) COLLAGENASE (MMP- 1); 1FBL 4 CHAIN: NULL; 1FBL 5	METALLOPROTEASE
958	1fb1		121	487	0			592.38	FIBROBLAST (INTERSTITIAL) COLLAGENASE (MMP- 1); 1FBL 4 CHAIN: NULL; 1FBL 5	METALLOPROTEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
958	1fbl		74	188	7e-58			57.48	IFBL 5 FIBROBLAST (INTERSTITIAL) COLLAGENASE (MMP-1); IFBL 4 CHAIN: NULL; IFBL 5	METALLOPROTEASE
958	1hfc		128	282	1.4e-70	1.08	1.00		METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) IHFC 3	
958	1hfc		128	284	1.4e-70			274.25	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) IHFC 3	
958	1hfc		81	188	5.6e-55			168.69	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) IHFC 3	
958	1lbu		50	127	0.0014	0.42	0.24		MURAMOYL- PENTAPEPTIDE CARBOXYPEPTIDASE; CHAIN: NULL;	HYDROLASE HYDROLASE, NUCLEAR RECEPTOR, CARBOXYPEPTIDASE
958	1sat		47	490	1.4e-34			78.13	SERRATIA PROTEASE ISAT 3	HYDROLASE (SERINE PROTEASE) SERRALYSIN, MAJOR METALLO PROTEASE FROM ISAT 4 PARALLEL BETA HELIX, PARALLEL BETA ROLL ISAT 7
958	1sat		83	406	1.4e-34	0.21	0.39		SERRATIA PROTEASE ISAT 3	HYDROLASE (SERINE PROTEASE) SERRALYSIN, MAJOR METALLO PROTEASE FROM ISAT 4 PARALLEL BETA HELIX, PARALLEL BETA ROLL ISAT 7
958	1sim		54	285	1.1e-96	0.76	1.00		STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3;

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION
958	1slm		55	285	1.1e-96			271.16	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION
958	1slm		8	187	2.8e-83			190.20	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION
962	1ap0		35	106	3e-14			50.89	MODIFIER PROTEIN 1; CHAIN: NULL;	CHROMATIN-BINDING MOMOD1, HETEROCHROMATIN PROTEIN 1; CHROMATIN-BINDING, PROTEIN INTERACTION MOTIF, ALPHA+BETA
964	1a0q	L	20	242	8.4e-66			110.96	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
964	1a2y	A	1	101	9.8e-39			51.49	MONOCLONAL ANTIBODY D1.3; CHAIN: A, B; LYSOZYME; CHAIN: C;	COMPLEX (IMMUNOGLOBULIN/HYDROLAS E) COMPLEX (IMMUNOGLOBULIN/HYDROLAS E), IMMUNOGLOBULIN V2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/ROL D score	Compound	PDB annotation
964	1a7q	L	1	101	4.2e-37			53.02	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, VARIANT
964	1adq	L	21	246	8.4e-72			111.15	IGG4 REA; CHAIN: A; RF-ANIGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
964	1ae6	L	19	243	2.8e-65			107.14	ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
964	1afv	H	24	239	5.6e-85	0.22	-1202.08		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
964	1ahw	A	19	243	2.8e-71			109.26	IMMUNOGLOBULIN FAB 5G9; CHAIN: A, B, D, E; TISSUE FACTOR; CHAIN: C, F;	COMPLEX (IMMUNOGLOBULIN/TISSUE FACTOR) FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN; TF, THROMBOPLASTIN, COAGULATION FACTOR III; BLOOD COAGULATION, TISSUE FACTOR, FAB, COMPLEX, ANTIBODY, 2 COMPLEX (IMMUNOGLOBULIN/TISSUE FACTOR)
964	1aif	A	19	245	5.6e-69			107.73	ANTI-IDiotYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
964	1aql	L	21	246	2.8e-68			110.74	FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
964	1ay1	L	19	238	7e-72			111.56	TP7 FAB; CHAIN: L, H;	AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
										IMMUNOGLOBULIN
964	1b0w	A	1	101	4.2e-45			50.86	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
964	1baF	L	19	243	1.4e-71			107.96	IMMUNOGLOBULIN FAB FRAGMENT OF MURINE MONOCLONAL ANTIBODY AN02 COMPLEX IBAF 3 WITH ITS HAPTEN (2,2,6,6-TETRAMETHYL-1-PIPERIDINYLOXY- IBAF 4 DINITROPHENYL) IBAF 5	
964	1bj1	J	19	242	2.8e-74			107.19	FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
964	1bjm	A	20	246	1.4e-66			115.09	LOC - LAMBDA I TYPE LIGHT-CHAIN DIMER; IBJM 6 CHAIN: A, B; IBJM 7	IMMUNOGLOBULIN BENCE-JONES PROTEIN; IBJM 8 BENCE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES IBJM 13
964	1bvk	A	1	101	1.1e-44			52.15	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
964	1bw w	A	1	101	4.2e-47			50.82	IG KAPPA CHAIN V-L REGION RE; CHAIN: A, B;	ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
964	1c1g	A	1	234	8.4e-43			63.76	TROPOMYOSIN; CHAIN: A, B, C, D	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENGE-JONES 2 PROTEIN, IMMUNE SYSTEM CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
964	1d5i	L	19	238	9.8e-69			108.44	CHIMERIC GERMLINE PRECURSOR OF OXY- COPE CHAIN: L; CHIMERIC GERMLINE PRECURSOR OF OXY- COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
964	1e4x	H	24	238	1.3e-81	0.14	-1202.08		TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN- PEPTIDE RECOGNITION
964	1e6o	H	24	239	5.6e-82	0.22	-1202.08		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA
964	1f8t	L	19	243	2.8e-65			107.82	ANTIBODY FAB FRAGMENT (LIGHT CHAIN); CHAIN: L; ANTIBODY FAB FRAGMENT (HEAVY CHAIN); CHAIN: H	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING FRAGMENT, INTERLEUKIN-2 2, X-RAY ANALYSIS, CRYSTAL
964	1fbi	H	24	239	2.8e-81	0.07	-1202.08		COMPLEX	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY F9.13.7 (IGG1) 1FBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) 1FBI 4	
964	1fgn	H	24	238	2.8e-83	0.25	-1202.08		IMMUNOGLOBULIN FAB 5G9; CHAIN: L, H;	IMMUNOGLOBULIN FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN; ANTIBODY, FAB, ANTI-TF, MONOCLONAL, MURINE, IMMUNOGLOBULIN
964	1fj1	A	19	242	5.6e-68			113.25	HYBRIDOMA ANTIBODY LA2 (LIGHT CHAIN); CHAIN: A, C; HYBRIDOMA ANTIBODY LA2 (HEAVY CHAIN); CHAIN: B, D; OUTER SURFACE PROTEIN A; CHAIN: E, F;	IMMUNE SYSTEM LA2 FAB; LA2 FAB; OSP A, OSP A, LYME DISEASE, ANTIBODY FAB FRAGMENT, NEUTRALIZING 2 EPTOPE
964	1fhs	L	19	243	9.8e-71			107.73	IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN TBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
964	1hi6	A	19	243	1.3e-66			109.95	IGG2A KAPPA ANTIBODY CB41 (LIGHT CHAIN); CHAIN: A; IGG2A KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSSREACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
964	1hxm	B	19	243	9e-57			242.19	GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C, E, G; GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T-CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GDTOR
964	1hxm	B	1	84	8.4e-34			50.67	GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C, E, G; GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T-CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GDTOR
964	1hzh	H	25	296	2.8e-83	0.11	-1202.08		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
964	1igt	B	145	296	1.4e-12	0.14	-1202.08		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
964	1igt	B	24	283	8.4e-90	0.06	-1202.08		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
964	1kb5	L	19	243	2.8e-70			109.47	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2
964	1lil	A	22	246	4.2e-69			114.77	LAMBDA III BENGE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN (IMMUNOGLOBULIN/RECEPTOR)
964	1ngp	H	24	239	2.8e-82	0.09	-1202.08		NI G9 (GGI=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN JONES PROTEIN IMMUNOGLOBULIN, BENGE JONES PROTEIN IMMUNOGLOBULIN, IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
964	1wtl	A	1	101	4.2e-45			50.35	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
964	25c8	H	24	239	4.2e-83	0.12	-1202.08		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
964	2fb4	L	20	246	4.2e-67			109.74	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB 2FB4 4	
964	2mcg	1	20	246	9.8e-69			108.78	IMMUNOGLOBULIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (/MCG\$) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
964	8fab	A	23	241	1.4e-69			118.67	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
968	1cdo	A	157	495	1.4e-78			91.38	ALCOHOL DEHYDROGENASE; 1CDO 6 CHAIN: A, B; 1CDO 7	OXIDOREDUCTASE (CH-OH(D)-NAD(A)) OXIDOREDUCTASE 1CDO 15
968	1cdo	A	164	492	1.4e-78	0.33	-1202.08		ALCOHOL DEHYDROGENASE; 1CDO 6 CHAIN: A, B; 1CDO 7	OXIDOREDUCTASE (CH-OH(D)-NAD(A)) OXIDOREDUCTASE 1CDO 15
968	1cdo	A	1	327	2.8e-69			82.11	ALCOHOL	OXIDOREDUCTASE (CH-OH(D)-

Table 5

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DEHYDROGENASE, ICDO 6 CHAIN: A, B; ICDO 7	NAD(A)) OXIDOREDUCTASE ICDO 15
968	Idlt	A	157	495	1.1e-80			92.65	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD
968	Idlt	A	164	492	1.1e-80	0.32	-1202.08		ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD
968	Idlt	A	3	327	5.6e-72			81.94	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD
968	Idch	A	110	495	8.4e-87			100.84	HUMAN BETAI ALCOHOL DEHYDROGENASE; IDEH 7 CHAIN: A, B; IDEH 8	OXIDOREDUCTASE BETAI ADH; IDEH 9 NAD+ DEPENDENT ALCOHOL DEHYDROGENASE IDEH 26
968	Idch	A	164	492	8.4e-87	0.41	-1202.08		HUMAN BETAI ALCOHOL DEHYDROGENASE; IDEH 7 CHAIN: A, B; IDEH 8	OXIDOREDUCTASE BETAI ADH; IDEH 9 NAD+ DEPENDENT ALCOHOL DEHYDROGENASE IDEH 26
968	Idch	A	1	327	1.4e-78			87.63	HUMAN BETAI ALCOHOL DEHYDROGENASE; IDEH 7 CHAIN: A, B; IDEH 8	OXIDOREDUCTASE BETAI ADH; IDEH 9 NAD+ DEPENDENT ALCOHOL DEHYDROGENASE IDEH 26
968	Ie3i	A	106	495	7e-74			100.96	ALCOHOL DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE ALCOHOL DEHYDROGENASE
968	Ie3i	A	164	492	7e-74	0.38	-1202.08		ALCOHOL	ALCOHOL DEHYDROGENASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
968	1e3i	A	3	327	5.6e-67			82.29	DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE
968	1e3j	A	163	491	1.4e-60			82.26	DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE
968	1e3j	A	1	323	2.8e-58			78.55	NADP(H)-DEPENDENT KETOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE, FRUCTOSE REDUCTION
968	1het	A	110	495	4.2e-83			94.36	NADP(H)-DEPENDENT KETOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE OXIDOREDUCTASE, FRUCTOSE REDUCTION
968	1het	A	164	492	4.2e-83	0.46	-1202.08		ALCOHOL DEHYDROGENASE E CHAIN; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I; OXIDOREDUCTASE(NAD(A)-CHOH(D))
968	1het	A	3	327	2.8e-75			79.40	ALCOHOL DEHYDROGENASE E CHAIN; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE I; OXIDOREDUCTASE(NAD(A)-CHOH(D))
968	1hso	A	110	495	7e-87			101.16	CLASS I ALCOHOL DEHYDROGENASE 1, ALPHA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), ALPHA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE
968	1hso	A	164	492	7e-87	0.46	-1202.08		CLASS I ALCOHOL DEHYDROGENASE 1, ALPHA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), ALPHA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE
968	1hso	A	1	327	1.4e-78			89.46	CLASS I ALCOHOL DEHYDROGENASE 1, ALPHA SUBUNIT;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), ALPHA ROSSMANN FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
968	1ht0	A	110	495	4.2e-86			105.32	CHAIN: A, B; CLASS I ALCOHOL DEHYDROGENASE 3, GAMMA SUBUNIT; CHAIN: A, B;	ALCOHOL DEHYDROGENASE OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), GAMMA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE, ZINC
968	1ht0	A	164	492	4.2e-86	0.33	-1202.08		CLASS I ALCOHOL DEHYDROGENASE 3, GAMMA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), GAMMA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE, ZINC
968	1ht0	A	3	327	4.2e-78			90.30	CLASS I ALCOHOL DEHYDROGENASE 3, GAMMA SUBUNIT; CHAIN: A, B;	OXIDOREDUCTASE ALCOHOL DEHYDROGENASE (CLASS I), GAMMA ROSSMANN FOLD, ALCOHOL DEHYDROGENASE, ZINC
968	1kev	A	1	325	9.8e-48			66.86	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP
968	1qor	A	165	495	2.8e-77			132.05	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 1QOR 3	
968	1qor	A	168	493	2.8e-77	0.62	-1202.08		OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 1QOR 3	
968	1qor	A	2	327	5.6e-78			128.24	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
968	1tcf		11	162	0.008			52.38	NADPH 100R 3 TROPONIN C ₂ CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
968	1teh	A	112	495	1.4e-90			100.75	HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
968	1teh	A	164	492	1.4e-90	0.37	-1202.08		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE
968	1teh	A	3	327	4.2e-78			85.11	HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
968	1ykf	A	165	494	2.8e-58			68.99	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	DEHYDROGENASE
968	1ykf	A	1	326	1.4e-49			67.17	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE
968	7adh		1	327	5.6e-60			62.04	OXIDOREDUCTASE (NAD(A)-CHOH(D)) ISONICOTINIMIDYLATE D LIVER ALCOHOL DEHYDROGENASE 7ADH 4 (E.C.1.1.1.1) 7ADHD 1 7ADHD 2	OXIDOREDUCTASE
970	1bfd		14	349	4.2e-39	0.14	-1202.08		BENZOYLFORMATE DECARBOXYLASE; CHAIN: NULL;	LYASE LYASE, CARBON-CARBON, DECARBOXYLASE, MANDELATE CATABOLISM, 2
970	1dtw	A	1	316	8.4e-70			118.95	BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: A; BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: B;	OXIDOREDUCTASE THDP-BINDING FOLD, BRANCHED-CHAIN ALPHA-KETO ACID 2 DEHYDROGENASE
970	1dtw	A	73	453	5.6e-70			161.96	BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: A; BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: B;	OXIDOREDUCTASE THDP-BINDING FOLD, BRANCHED-CHAIN ALPHA-KETO ACID 2 DEHYDROGENASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
970	1dlw	A	77	449	5.6e-70	0.44	-1202.08		BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: A; BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE CHAIN: B;	OXIDOREDUCTASE, THDP-BINDING FOLD, BRANCHED-CHAIN ALPHA-KETO ACID 2 DEHYDROGENASE
970	1pox	A	15	392	7e-40	0.22	-1202.08		OXIDOREDUCTASE(OXYGEN AS ACCEPTOR) PYRUVATE OXIDASE (E.C.1.2.3.3) MUTANT WITH PRO 178 IPOX 3 REPLACED BY SER, SER 188 REPLACED BY ASN, AND ALA 458 IPOX 4 REPLACED BY VAL (P178S,S188N,A458V) IPOX 5	
970	1pyd	A	15	365	1.3e-46	0.06	-1202.08		LYASE (CARBON-CARBON) PYRUVATE DECARBOXYLASE (PDC) (E.C.4.1.1.1) IPVD 3	
970	1qso	A	121	446	2.8e-59	0.61	-1202.08		2-OXOISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2-OXOISOVALERATE DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE
970	1qso	A	1	317	2.8e-59			91.32	2-OXOISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2-OXOISOVALERATE	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	
970	1qso	A	40	446	9e-76			140.12	2-OXOISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2- OXOISOVALERATE DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE
970	1qso	A	68	445	9e-76	0.55	-1202.08		2-OXOISOVALERATE DEHYDROGENASE ALPHA-SUBUNIT; CHAIN: A; 2- OXOISOVALERATE DEHYDROGENASE BETA-SUBUNIT; CHAIN: B;	OXIDOREDUCTASE HETEROTETRAMER, THDP COFACTOR, OXIDOREDUCTASE
970	1tkk	A	127	446	3e-57	0.16	-1202.08		TRANSFERRASE(KETONE RESIDUES) TRANSKETOLASE (E.C.2.2.1.1) TRK 3	
971	1a4j	A	24	139	1e-08	0.14	-1202.08		IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
971	1bd2	E	32	180	1.4e-67	0.07	-1202.08		HLA-A-0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
971	1bd2	E	32	180	1.4e-67			86.31	CHAIN: E; HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
971	1bec		32	180	5.6e-66			81.96	14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
971	1d9k	B	1	96	8.4e-38			57.60	T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A, E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B, F; MHC I-AK A CHAIN (ALPHA CHAIN); CHAIN: C, G; MHC I-AK B CHAIN (BETA CHAIN); CHAIN: D, H; CONALBUMIN PEPTIDE; CHAIN: P, Q;	IMMUNE SYSTEM MHC I-AK; MHC I-AK; T-CELL RECEPTOR, MHC CLASS II, D10, I-AK
971	1fyt	E	32	180	5.6e-61			81.57	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-	IMMUNE SYSTEM HLA-DR1, DRA; HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CELL RECEPTOR BETA CHAIN; CHAIN: E;	
971	InfJ	B	30	180	7e-64	0.19	-1202.08		N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGL OBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGL OBULIN)
971	InfJ	B	30	180	7e-64			124.34	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGL OBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGL OBULIN)
971	1ter	B	30	180	1.3e-64	0.11	-1202.08		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
971	1ter	B	30	180	1.3e-64			73.51	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
972	1eun	A	21	239	0.003			62.32	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
975	1ej	A	163	485	1.4e-18	0.07	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
975	1ej	A	182	532	9.8e-23			85.09	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
975	1ej	A	212	527	9.8e-23	0.18	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
975	1ej	A	410	580	2.8e-19	0.02	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1;	TRANSCRIPTION INHIBITOR BETA-PROPELLER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
975	1got	B	227	567	1.4e-20			85.50	CHAIN: A, B, C; GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
975	1got	B	305	579	1.4e-20	0.06	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT- GAMMA; CHAIN: G;	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
977	1cvu	A	108	710	9.8e-91			142.67	PROTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROTAGLANDIN, ARACHIDONATE, 2 ENDOPEROXIDE
977	1cvu	A	155	631	9.8e-91	0.02	-1202.08		PROTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROTAGLANDIN, ARACHIDONATE, 2 ENDOPEROXIDE
977	1cvu	A	6	584	0			142.21	PROTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9-MER; CHAIN: F;	OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROTAGLANDIN, ARACHIDONATE, 2 ENDOPEROXIDE
977	1d2v	A	132	235	1.5e-42			141.84	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE;	OXIDOREDUCTASE HEME- PROTEIN, PEROXIDASE, OXIDOREDUCTASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
977	1d2v	A	6	109	2.8e-42			141.89	CHAIN: C, D; MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	PEROXIDASE-2 BROMIDE COMPLEX OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
977	1d2v	C	244	733	0			561.59	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
977	1d2v	C	246	732	0	0.63	-1202.08		MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	OXIDOREDUCTASE HEME-PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
977	1eqg	A	108	710	1.4e-93			148.59	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A, B;	OXIDOREDUCTASE COX-1; EGF DOMAIN, NSAID BINDING, IBUPROFEN, MEMBRANE-BINDING 2 DOMAIN, CYCLOOXYGENASE, PEROXIDASE, OXIDOREDUCTASE, 3 DIOXYGENASE, PEROXIDASE
977	1eqg	A	1	584	2.8e-99			149.69	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A, B;	OXIDOREDUCTASE COX-1; EGF DOMAIN, NSAID BINDING, IBUPROFEN, MEMBRANE-BINDING 2 DOMAIN, CYCLOOXYGENASE, PEROXIDASE, OXIDOREDUCTASE, 3 DIOXYGENASE, PEROXIDASE
981	1a2y	A	34	146	4.2e-40			59.18	MONOCLONAL ANTIBODY D1.3; CHAIN:	COMPLEX (IMMUNOGLOBULIN/HYDROLAS

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B; LYSOZYME; CHAIN: C;	E) COMPLEX (IMMUNOGLOBULIN/HYDROLASE E), IMMUNOGLOBULIN V2 REGION, SIGNAL, HYDROLASE, GLYCOSIDASE, BACTERIOLYTIC 3 ENZYME, EGG WHITE
981	1a6v	H	34	150	1.1e-17			56.08	BI-8; CHAIN: L, H, M, I, N, J;	IMMUNOGLOBULIN, HAPTEN
981	1a7q	L	1	101	1.4e-31			50.53	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN
981	1a7q	L	34	146	1.4e-38			59.67	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN
981	1ad0	A	34	215	9.8e-60			55.26	FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN, FAB FRAGMENT
981	1adq	L	36	203	2.8e-68	0.25	-1202.08		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2
981	1a07	E	36	215	1.5e-12			61.51	HLA-A 0201; CHAIN: A; BETA-2	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2
									MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
981	1aqk	L	36	203	1.4e-62	0.10	-1202.08		FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
981	1ar1	D	34	146	1.4e-35			56.21	CYTOCHROME C OXIDASE; CHAIN: A, B; ANTIBODY FV FRAGMENT; CHAIN: C, D;	AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
981	1b0w	A	34	153	2.8e-43			55.87	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
981	1b2w	L	34	198	2.8e-62	0.16	-1202.08		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
981	1b6d	A	34	198	4.2e-62	0.10	-1202.08		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
981	1b62	D	35	214	7e-20			55.30	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
981	1bj1	J	34	198	9.8e-64	0.18	-1202.08		CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	
									FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
981	1bvk	A	34	146	1.4e-44			55.47	HULYSII; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
981	1bw w	A	32	147	5.6e-45			57.52	IG KAPPA CHAIN V-1 REGION REL; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENGE-JONES 2 PROTEIN, IMMUNE SYSTEM
981	1cel	L	34	215	8.4e-61			55.66	CAMPATH-1H;LIGHT CHAIN; CHAIN: L; CAMPATH-1H;HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
981	1dee	A	34	198	1.4e-63	0.23	-1202.08		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F;	IMMUNE SYSTEM FAB-1BP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
981	1dfb	L	34	215	5.6e-60			55.95	IMMUNOGLOBULIN 3D6 FAB 1DFB 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
981	1dm0	A	35	198	2.8e-62	0.25	-1202.08		IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN); CHAIN: A, C ₂ IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN); CHAIN: B, D ₂	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
981	1fgv	L	1	102	7e-41			50.49	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA FV) IFGV 4	
981	1fgv	L	34	146	1.3e-46			57.40	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 IFGV 3 ANTIBODY 'H52' (HUH52-AA FV) IFGV 4	
981	1hxm	B	34	215	4.2e-25			57.17	GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C ₂ E, G; GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T-CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GDTCTR
981	1igm	L	34	155	4.2e-46			59.49	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT IIGM3	
981	1jth	L	34	206	1.4e-45			56.13	ANTIBODY A6; CHAIN: L, H; INTERFERON-GAMMA RECEPTOR ALPHA CHAIN; CHAIN: I;	COMPLEX (ANTIBODY/ANTIGEN) CYTOKINE RECEPTOR, COMPLEX (ANTIBODY/ANTIGEN), 2 TRANSMEMBRANE, GLYCOPROTEIN
981	1lhl	A	36	203	8.4e-65	0.07	-1202.08		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
981	1ngp	H	34	215	4.2e-23			56.17	NIG9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,
981	1plg	H	34	215	2.8e-18			56.05	IGG2A=KAPPA=, 1PLG 4 CHAIN: L, H; 1PLG 5	IMMUNOGLOBULIN
981	1tcr	A	35	215	7e-20			57.82	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR, T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
981	2fgw	L	34	198	9.8e-64	0.07	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
981	2fgw	L	34	215	9.8e-64			56.05	IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
981	2pcp	B	34	215	9.8e-19			54.90	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN
981	8fab	A	38	203	4.2e-66	0.13	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
981	8fab	A	38	215	4.2e-66			55.65	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
982	12e8	L	24	224	1.4e-74			96.49	2E8 (IGG1=KAPPA=)	IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
982	1a4j	A	23	238	9.8e-72			98.04	ANTIBODY; CHAIN: L, H, M, P; IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
982	1a07	D	1	97	1.3e-35			70.96	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
982	1b2w	L	22	224	1.4e-81			98.81	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
982	1b6d	A	22	222	1.4e-81	0.00	-1202.08		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
982	1b6d	A	22	233	1.4e-81			96.63	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
982	1b88	A	1	97	1.1e-40			83.05	T CELL RECEPTOR V-ALPHA DOMAIN; CHAIN: A, B;	T CELL RECEPTOR TCR; T CELL RECEPTOR, MHC CLASS I, HUMAN IMMUNODEFICIENCY VIRUS, 2 MOLECULAR RECOGNITION

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
982	1bd2	D	22	218	3e-74			230.06	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
982	1bj1	J	22	223	1.1e-83	0.15	-1202.08		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
982	1ce1	L	22	232	1.4e-79			97.53	CAMPATH-1H/LIGHT CHAIN; CHAIN: L; CAMPATH-1H/HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
982	1c1c	A	24	224	1.4e-74			96.33	IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE
982	1d9k	A	1	97	2.8e-42			79.58	T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A, E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B, F; MHC I-AK A CHAIN (ALPHA CHAIN);	IMMUNE SYSTEM MHC I-AK; MHC I-AK; T-CELL RECEPTOR, MHC CLASS II, D10, I-AK

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: C, G; MHC I-AK B CHAIN (BETA CHAIN); CHAIN: D, H; CONALBUMIN PEPTIDE; CHAIN: P, Q;	
982	Idee	A	22	226	1.4e-84			96.48	IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
982	Idhp	A	12	304	5.6e-92			130.53	DIHYDRODIPICOLINATE SYNTHASE; CHAIN: A, B;	SYNTHASE DHDS; SYNTHASE, DIHYDRODIPICOLINATE
982	Idn0	A	22	223	2.8e-79	0.02	-1202.08		IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN); CHAIN: A, C; IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
982	Ie4x	L	22	224	1.4e-74			97.96	TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
982	Iegj	L	24	221	1.4e-73			100.34	CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR; CHAIN: A; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H	IMMUNE SYSTEM CYTOKINE RECEPTOR COMPLEXED TO AN ANTIBODY
982	Iemt	L	22	224	1.3e-75			98.73	IGG ANTIBODY (LIGHT CHAIN); CHAIN: L; IGG ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM ANTI-FULLERENE ANTIBODY, NANOTUBES

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
982	1f5g	L	21	224	7e-75			97.87	IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB FRAGMENT 1FIG 3	
982	1fms	L	22	224	8.4e-78			96.30	IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3, 2B VON WILLEBRAND DISEASE
982	1fvd	A	22	223	7e-81	0.31	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
982	1fyt	D	22	218	2.8e-57			204.11	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DR1, DR1, HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
982	1g9m	L	21	227	1.4e-77			97.48	ENVELOPE GLYCOPROTEIN GP120; CHAIN: G; T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: C; ANTIBODY 17B, LIGHT CHAIN;	VIRUS/VIRAL PROTEIN COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120 FROM LABORATORY-ADAPTED ISOLATE, HXB2, 3 SURFACE T-CELL GLYCOPROTEIN CD4,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
982	1i7z	A	24	224	2.8e-76			98.87	CHAIN: L; ANTIBODY 17B, HEAVY CHAIN; CHAIN: H; CHIMERA OF IG KAPPA CHAIN: HUMAN CONSTANT REGION CHAIN: A, C; CHIMERA OF IG GAMMA-1 CHAIN: HUMAN CONSTANT CHAIN: B, D;	ANTIGEN-BINDING FRAGMENT 4 OF HUMAN IMMUNOGLOBULIN 17B
982	1kb5	A	1	97	5.6e-43			87.06	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2
982	1qpn	D	23	221	1.2e-77			239.88	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; T-CELL RECEPTOR, ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR, BETA CHAIN; CHAIN: E;	(IMMUNOGLOBULIN/RECEPTOR) IMMUNE SYSTEM MHC CLASS I HLA-A; MHC CLASS I ANTIGEN; A6-TCR; TCR BETA CHAIN; HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T2 CELL RECEPTOR
982	2fgw	L	22	223	7e-83	0.04	-1202.08		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
983	1b6b	B	221	337	9.8e-10	0.35	-1202.08		ARYLAALKYLAMINE N-	TRANSFERASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ACETYLTRANSFERASE; CHAIN: A, B;	ACETYLTRANSFERASE
983	1c1w	A	221	337	1.1e-08	0.14	-1202.08		SEROTONIN N- ACETYLTRANSFERASE; CHAIN: A;	TRANSFERASE N-ACETYL TRANSFERASE
983	1ib1	B	221	337	1.1e-08	0.20	-1202.08		14-3-3 ZETA ISOFORM; CHAIN: A, B, C, D; SEROTONIN N- ACETYLTRANSFERASE; CHAIN: E, F, G, H;	SIGNALING PROTEIN/TRANSFERASE PROTEIN KINASE C INHIBITOR PROTEIN-1; ARALKYLAMINE N- ACETYLTRANSFERASE, AA-NAT, N-ACETYL TRANSFERASE, 14-3-3, SIGNAL TRANSDUCTION, PROTEIN-2 PROTEIN COMPLEX, PHOSPHORYLATION
983	1qsm	A	218	334	9.8e-14	0.03	-1202.08		HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE
985	1ext	A	38	209	1.4e-10			53.75	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
985	1ext	A	52	202	1.4e-10	0.25	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
985	1g44	A	44	258	3e-07			57.93	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
985	1g44	B	31	250	0.0006			60.13	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
985	1hdj		9	84	1.1e-29			70.79	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
985	1igr	A	40	171	1.5e-09	0.21	-1202.08		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
985	1klo		44	221	7e-13			55.87	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
985	1ncf	A	52	179	8.4e-09	0.15	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	SIGNALING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19
985	9wga	A	45	224	7e-14			51.43	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
987	1a4y	A	127	368	1.2e-40	0.46	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1a4y	A	246	375	1.2e-19	0.23	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1a4y	A	54	355	7.5e-45	0.39	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
987	1a9n	A	108	283	1.3e-28	0.31	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1a9n	A	179	330	1.4e-30	0.79	-1202.08		CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	203	355	1e-32	0.59	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	276	368	1.4e-15	0.31	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	54	213	1.5e-21	0.15	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	A	83	233	1.2e-29	0.46	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	108	283	1.5e-28	0.13	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	179	327	9e-31	0.73	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
									U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	203	355	6e-32	0.50	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1a9n	C	273	369	1.5e-15	0.36	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	54	233	9e-22	0.11	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1a9n	C	83	231	1.5e-29	0.50	-1202.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
987	1d0b	A	110	329	4.5e-37			71.98	INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	170	368	7.5e-34	1.01	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	244	423	1.3e-20	0.78	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	279	433	5.6e-15	0.33	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	33	204	7e-22	0.30	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	48	232	3e-27	0.29	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	61	279	4.5e-37	0.63	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
987	1d0b	A	63	252	2.8e-26	0.41	-1202.08		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1dce	A	272	381	2.8e-13	0.56	-1202.08		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	REPEAT, CALCIUM BINDING, CELL ADHESION TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
987	1fo1	B	228	369	9e-17	0.07	-1202.08		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFXD); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
987	1fqv	A	183	380	9e-20	0.25	-1202.08		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
987	1fqv	A	71	400	7.5e-25			69.13	SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
987	1fs2	A	187	385	3e-15	0.13	-1202.08		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
987	1fs2	A	53	321	1.5e-18	0.03	-1202.08		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19, SKP1, SKP2, F-BOX, LRKS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
987	1yr8	A	126	371	7.5e-28	0.12	-1202.08		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	1yr8	A	57	390	9e-34			70.31	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	1yr8	A	59	185	3e-14	0.21	-1202.08		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	1yr8	A	75	282	3e-29	0.33	-1202.08		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
987	1yr6	A	94	330	9e-34	0.48	-1202.08		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
987	2bnh		80	368	1.5e-48	0.52	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE INHIBITOR,
988	1ep2	A	103	359	1.4e-58	0.45	-1202.08		NITROGENASE IRON PROTEIN; CHAIN: A, B;	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
988	1ep2	A	104	359	1.4e-58			64.61	NITROGENASE IRON PROTEIN; CHAIN: A, B;	OXIDOREDUCTASE CP2; OXIDOREDUCTASE, NITROGENASE IRON PROTEIN HEADER CONNECT LINK
988	1fp6	A	100	359	9.8e-61			58.49	NITROGENASE IRON PROTEIN; CHAIN: A, B, C, D;	OXIDOREDUCTASE CP2; OXIDOREDUCTASE, NITROGENASE IRON PROTEIN HEADER CONNECT LINK
988	1fp6	A	103	359	9.8e-61	0.36	-1202.08		NITROGENASE IRON	OXIDOREDUCTASE COMPONENT II, NITROGENASE REDUCTASE, NITROGENASE, NITROGEN FIXATION, NUCLOTIDE, MGADP, FE 2 PROTEIN, AV2
988	1fp6	A	103	359	9.8e-61	0.36	-1202.08		NITROGENASE IRON	OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
988	1fp6	A	104	359	3e-46	0.35	-1202.08		PROTEIN; CHAIN: A, B, C, D;	NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGENASE, NITROGEN FIXATION, NUCLOTIDE, MGADP, FE 2 PROTEIN, AV2
988	1fts		19	296	1.1e-06			53.22	FTSY; CHAIN: NULL;	OXIDOREDUCTASE
988	1g20	E	103	359	1.4e-57	0.22	-1202.08		NITROGENASE	NITROGENASE COMPONENT I, DINITROGENASE, NIFD, NITROGENASE COMPONENT I, DINITROGENASE, NIFK, NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGEN-FIXATION, FE PROTEIN, MOFE PROTEIN, P-CLUSTER AND 2 FEMO COFACTOR
988	1g20	E	104	359	1.4e-57			62.01	NITROGENASE	OXIDOREDUCTASE
									MOLYBDENUM-IRON PROTEIN ALPHA CHAIN; CHAIN: A, C;	NITROGENASE COMPONENT I, DINITROGENASE, NIFD, NITROGENASE COMPONENT I, DINITROGENASE, NIFK, NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGEN-FIXATION, FE
									MOLYBDENUM-IRON PROTEIN BETA CHAIN; CHAIN: B, D;	PROTEIN, MOFE PROTEIN, P-CLUSTER AND 2 FEMO COFACTOR

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQ/OL ID score	Compound	PDB annotation
988	1g20	E	104	359	4.5e-48	0.58	-1202.08		NITROGENASE IRON PROTEIN; CHAIN: E, F, G, H;	PROTEIN, MOFE PROTEIN, P-CLUSTER AND 2 FEMO COFACTOR
988	1g3q	A	101	350	2.8e-48	0.54	-1202.08		NITROGENASE MOLYBDENUM-IRON PROTEIN ALPHA CHAIN; CHAIN: A, C;	OXIDOREDUCTASE NITROGENASE COMPONENT I, DINITROGENASE, NIFD; NITROGENASE COMPONENT I, DINITROGENASE, NIFK; NITROGENASE COMPONENT II, NITROGENASE REDUCTASE, NITROGEN-FIXATION, FE PROTEIN, MOFE PROTEIN, P-CLUSTER AND 2 FEMO COFACTOR
988	1g3q	A	101	354	2.8e-48			104.71	CELL DIVISION INHIBITOR; CHAIN: A;	CELL CYCLE, HYDROLASE MIND ATPASE; ALPHA-BETA-ALPHA LAYERED, PROTEIN-ADP COMPLEX
988	1hyq	A	102	351	9.8e-46			105.60	CELL DIVISION INHIBITOR (MIND-1); CHAIN: A;	CELL CYCLE, HYDROLASE MIND ATPASE; ALPHA-BETA-ALPHA LAYERED, PROTEIN-ADP COMPLEX
988	1hyq	A	103	350	9.8e-46	0.31	-1202.08		CELL DIVISION INHIBITOR (MIND-1); CHAIN: A;	CELL CYCLE MIND; MING, FTSZ, BACTERIAL CELL DIVISION
988	1hyq	A	104	350	1.5e-39	0.70	-1202.08		CELL DIVISION INHIBITOR (MIND-1); CHAIN: A;	CELL CYCLE MIND; MING, FTSZ, BACTERIAL CELL DIVISION
988	1j8m	F	26	298	7e-17			50.31	SIGNAL RECOGNITION 54 KDA PROTEIN; CHAIN: F;	SIGNALING PROTEIN SRP54; SIGNALING PROTEIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
988	1n2c	E	100	359	9.8e-61			64.02	NITROGENASE MOLYBDENUM-IRON PROTEIN; CHAIN: A, B, C, D; NITROGENASE IRON PROTEIN; CHAIN: E, F, G, H;	COMPLEX OF NITROGENASE PROTEINS NITROGENASE COMPONENT I, DINITROGENASE; NITROGENASE COMPONENT II, NITROGENASE REDUCTASE; NITROGENASE, NITROGEN FIXATION, SIGNAL TRANSDUCTION, 2 ELECTRON TRANSFER, ATP HYDROLYSIS, COMPLEX OF NITROGENASE 3 PROTEINS
988	1n2c	E	103	359	9.8e-61	0.41	-1202.08		NITROGENASE MOLYBDENUM-IRON PROTEIN; CHAIN: A, B, C, D; NITROGENASE IRON PROTEIN; CHAIN: E, F, G, H;	COMPLEX OF NITROGENASE PROTEINS NITROGENASE COMPONENT I, DINITROGENASE; NITROGENASE COMPONENT II, NITROGENASE REDUCTASE; NITROGENASE, NITROGEN FIXATION, SIGNAL TRANSDUCTION, 2 ELECTRON TRANSFER, ATP HYDROLYSIS, COMPLEX OF NITROGENASE 3 PROTEINS
989	1aut	L	605	684	1.4e-11	0.03	-1202.08		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
989	1ccv	A	628	682	1.3e-14	0.42	-1202.08		CHYMOTRYPSIN INHIBITOR; CHAIN: A;	HYDROLASE INHIBITOR AMCI PROTEIN INHIBITOR, HEMOLYMPH, APIS MELLIFFERA, CANONICAL 2 INHIBITOR
989	1dva	L	146	229	5.6e-11	0.04	-1202.08		DES-GLA FACTOR VIIA	HYDROLASE/HYDROLASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
989	1fak	L	182	259	4.2e-12	0.02	-1202.08		(HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	INHIBITOR PROTEIN-PEPTIDE COMPLEX
989	1fak	L	182	259	4.2e-12	0.02	-1202.08		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX/SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, BGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
989	1hx2	A	628	682	9e-18	0.33	-1202.08		BST1; CHAIN: A;	HYDROLASE INHIBITOR BOMBINA SKIN TRYPSIN INHIBITOR BETA-SHEET DISULFIDE-RICH
989	1qub	A	89	364	6e-15	0.05	-1202.08		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHL, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
992	1a3r	L	20	221	9.8e-83	0.69	-1202.08		IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
992	1aqk	L	21	221	6e-86	0.91	-1202.08		FAB B7-15A2; CHAIN: L, H;	PEPTIDE) IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
992	1aqk	L	21	222	6e-86			232.04	FAB B7-15A2; CHAIN: L, H;	IMMUNOGLOBULIN HUMAN FAB, ANTI-TETANUS TOXOID, HIGH AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
992	1bjm	A	20	222	3e-83			228.10	LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; 1BJM 6 CHAIN: A, B; 1BJM 7	IMMUNOGLOBULIN BENGE-JONES PROTEIN; 1BJM 8 BENGE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES 1BJM 13
992	1bjm	A	21	221	1.3e-74	0.92	-1202.08		LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; 1BJM 6 CHAIN: A, B; 1BJM 7	IMMUNOGLOBULIN BENGE-JONES PROTEIN; 1BJM 8 BENGE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES 1BJM 13
992	1bjm	A	21	221	3e-83	1.01	-1202.08		LOC - LAMBDA 1 TYPE LIGHT-CHAIN DIMER; 1BJM 6 CHAIN: A, B; 1BJM 7	IMMUNOGLOBULIN BENGE-JONES PROTEIN; 1BJM 8 BENGE JONES, ANTIBODY, MULTIPLE QUATERNARY STRUCTURES 1BJM 13
992	1dzb	A	3	129	1.4e-44	0.74	-1202.08		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N- ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQRES ID score	Compound	PDB annotation
992	1hil	A	20	221	4.2e-83	0.76	-1202.08		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) 1HIL 3	
992	1hil	A	20	222	4.2e-83			155.83	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) 1HIL 3	
992	1ifh	L	20	221	4.2e-83	0.78	-1202.08		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX WITH PEPTIDE OF 1IFH 3 INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 101-107) 1IFH 4	
992	1ifh	L	20	222	4.2e-83			155.98	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) COMPLEX WITH PEPTIDE OF 1IFH 3 INFLUENZA HEMAGGLUTININ HA1 (STRAIN X47) (RESIDUES 101-107) 1IFH 4	
992	1nqb	A	12	130	1.4e-45	0.93	-1202.08		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
992	1gok	A	12	129	7e-46	1.09	-1202.08		MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
992	1sbs	L	20	221	1.4e-84	0.73	-1202.08		MONOCLONAL	MONOCLONAL ANTIBODY

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
992	1sbs	L	20	222	1.4e-84			158.44	ANTIBODY 3A2; CHAIN: H, L; MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
992	2fb4	L	20	221	7e-77	0.96	-1202.08		IMMUNOGLOBULIN 2FB4 4 IMMUNOGLOBULIN FAB	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
992	2fb4	L	20	222	7e-77			238.13	IMMUNOGLOBULIN 2FB4 4 IMMUNOGLOBULIN FAB	
992	2mcg	1	1	98	4.2e-51			88.32	IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCGS) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
992	2mcg	1	20	222	1.3e-82			268.98	IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCGS) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
992	2mcg	1	21	221	1.3e-82	0.86	-1202.08		IMMUNOGLOBULIN LAMBDA LIGHT CHAIN DIMER (MCGS) 2MCG 3 (TRIGONAL FORM) 2MCG 4	
992	7fab	L	20	222	4.5e-78			203.84	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
992	7fab	L	21	221	4.5e-78	0.91	-1202.08		IMMUNOGLOBULIN	

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
994	12e8	L	28	215	4.2e-09			63.88	IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	IMMUNOGLOBULIN IMMUNOGLOBULIN
994	1a4j	A	28	232	5.6e-11			63.22	IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
994	1ad0	A	28	234	5.6e-13			64.06	FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
994	1b2w	L	28	234	2.8e-11			68.36	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
994	1b4j	L	28	232	5.6e-13			68.55	ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
994	1b1h	A	2	306	1.4e-40	0.04	-1202.08		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
994	1cdy		37	213	3e-29	0.19	-1202.08		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
994	1cs6	A	1	308	3e-55			102.00	AXONIN-1; CHAIN: A;	TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
994	1cs6	A	22	304	3e-55	0.30	-1202.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
994	1cs6	A	2	307	9.8e-48	0.10	-1202.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
994	1cvs	C	127	306	9.8e-46	0.16	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1cvs	C	19	229	4.2e-29			63.89	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1cvs	C	217	337	7e-23	0.10	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1cvs	D	127	306	9.8e-44	0.13	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
994	1cvs	D	19	213	1.3e-29			73.52	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1cvs	D	217	337	7e-23	0.18	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1cvs	D	217	337	7e-23	0.18	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
994	1d5i	L	28	231	1.4e-12			63.72	CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
994	1dgi	R	8	304	7.5e-48			75.15	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
994	1eaj	A	36	127	3e-14	0.22	-1202.08		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOIL D score	Compound	PDB annotation
994	1epf	A	130	298	9e-30	0.21	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
994	1epf	A	135	290	7e-22	0.19	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
994	1epf	A	29	213	1.1e-34			82.22	NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
994	1epf	A	37	213	1.1e-34	0.28	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
994	1ev2	B	20	213	6e-29			71.72	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
994	1ev2	G	128	310	4.2e-44	0.22	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
994	1ev2	G	20	217	3e-30			70.77	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
994	1ev2	G	30	217	3e-30	0.02	-1202.08		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
994	1evt	C	19	213	9.8e-30			76.08	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
994	1f2q	A	129	307	1.5e-32	0.18	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
994	1f6a	A	125	307	1.5e-37	0.19	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
994	1f97	A	128	315	9e-37			78.34	JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
994	1f97	A	129	304	9e-37	0.17	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
994	1f97	A	136	301	1.4e-28	0.19	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
994	1f97	A	31	203	8.4e-29	0.05	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
994	1fcg	A	128	304	6e-35	0.07	-1202.08		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
994	1fcg	A	25	215	1.5e-24			64.84	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
994	1fcg	A	37	214	1.5e-24	0.13	-1202.08		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
994	1fhl	A	125	309	3e-36	0.11	-1202.08		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
994	1fsk	B	28	215	1.1e-10			64.25	MAJOR POLLEN ALLERGEN BET V 1-A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L;	IMMUNE SYSTEM BET V 1-A, BETV ALLERGEN; BV16 FAB- FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
994	1g9m	L	28	232	1.4e-11			64.69	ENVELOPE GLYCOPROTEIN GP120; CHAIN: G; T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: C; ANTIBODY	VIRUS/VIRAL PROTEIN COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120 FROM LABORATORY-ADAPTED ISOLATE, HXB2, 3 SURFACE T-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									17B, LIGHT CHAIN; CHAIN: L; ANTIBODY 17B, HEAVY CHAIN; CHAIN: H; MUTANT AL2 6E7S9G; CHAIN: A;	CELL GLYCOPROTEIN CD4, ANTIGEN-BINDING FRAGMENT 4 OF HUMAN IMMUNOGLOBULIN 17B
994	1h8n	A	27	245	1.4e-10			64.09	NEURAL CELL ADHESION MOLECULE; CHAIN: A;	ANTIBODY ANTIBODY, FRAMEWORK
994	1ie5	A	19	128	2.8e-15	0.15	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE
994	1ie5	A	207	304	1.3e-22	0.22	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	IMMUNOGLOBULIN FOLD CELL ADHESION N-CAM; INTERMEDIATE
994	1iil	G	128	310	1.1e-44	0.08	-1202.08		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN FOLD GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF- 2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE
994	1iil	G	30	217	7.5e-28	0.07	-1202.08		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	DOMAIN, B-TREFOIL GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF- 2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE
994	1ibb	B	30	309	1.5e-48			72.20	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
994	1lko		26	126	4.2e-12	0.09	-1202.08		TWITCHIN; CHAIN:	KINASE KINASE, TWITCHIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
994	Inct		30	126	1.3e-14	0.03	-1202.08		NULL; TTTN; CHAIN: NULL;	INTRASTERIC REGULATION MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
994	Inkr		129	301	3e-27	0.29	-1202.08		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
994	Immm		30	126	1.3e-14	0.19	-1202.08		MUSCLE PROTEIN TTTIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
994	2dli	A	128	301	1.5e-28	0.06	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
994	2feb	A	128	307	3e-35	0.10	-1202.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
994	2feb	A	25	217	1.5e-25			67.36	FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
994	3fct	A	28	233	4.2e-12			64.42	METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C, METAL	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE 2 SYSTEM
994	3hfm	H	28	215	4.2e-10			65.01	COMPLEX(ANTIBODY-ANTIGEN) IG*G1 FAB FRAGMENT (HY/HEL\$-10) AND LYSOZYME (E.C.3.2.1.17) 3HFM 4 COMPLEX 3HFM 5	
995	1c1g	A	1	245	1.3e-25			61.11	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
995	1cfe		30	177	2.8e-35	0.52	-1202.08		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
995	1cfe		30	177	7.5e-40			91.26	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
995	1cfe		32	177	7.5e-40	0.74	-1202.08		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1
995	1ij2	J	1	132	2.8e-46			114.02	23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A;	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L3; CHAIN: B;	PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10; 50S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN P0, HMAL10, L10E; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEIN L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA RIBOSOME ASSEMBLY, RNA-
									RIBOSOMAL PROTEIN L4; CHAIN: C;	
									RIBOSOMAL PROTEIN L5; CHAIN: D;	
									RIBOSOMAL PROTEIN L6; CHAIN: E;	
									RIBOSOMAL PROTEIN L7AE; CHAIN: F;	
									RIBOSOMAL PROTEIN L10; CHAIN: G;	
									RIBOSOMAL PROTEIN L10E; CHAIN: H;	
									RIBOSOMAL PROTEIN L13; CHAIN: I;	
									RIBOSOMAL PROTEIN L14; CHAIN: J;	
									RIBOSOMAL PROTEIN L15; CHAIN: K;	
									RIBOSOMAL PROTEIN L15E; CHAIN: L;	
									RIBOSOMAL PROTEIN L18; CHAIN: M;	
									RIBOSOMAL PROTEIN L18E; CHAIN: N;	
									RIBOSOMAL PROTEIN L19E; CHAIN: O;	
									RIBOSOMAL PROTEIN L21E; CHAIN: P;	
									RIBOSOMAL PROTEIN L22; CHAIN: Q;	
									RIBOSOMAL PROTEIN L23; CHAIN: R;	
									RIBOSOMAL PROTEIN	

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									L24; CHAIN: S; RIBOSOMAL PROTEIN L24E; CHAIN: T; RIBOSOMAL PROTEIN L29; CHAIN: U; RIBOSOMAL PROTEIN L30; CHAIN: V; RIBOSOMAL PROTEIN L31E; CHAIN: W; RIBOSOMAL PROTEIN L32E; CHAIN: X; RIBOSOMAL PROTEIN L37AE; CHAIN: Y; RIBOSOMAL PROTEIN L37E; CHAIN: Z; RIBOSOMAL PROTEIN L39E; CHAIN: 1; RIBOSOMAL PROTEIN L44E; CHAIN: 2;	RNA, PROTEIN-RNA, PROTEIN- PROTEIN
995	1qnx	A	1	177	1.3e-39	0.37	-1202.08		VES V 5; CHAIN: A;	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
995	1whi		12	132	4.2e-52			71.98	RIBOSOMAL PROTEIN L14; CHAIN: NULL;	RIBOSOMAL PROTEIN RIBOSOMAL PROTEIN, RRNA- BINDING
996	1os6	A	55	417	2.8e-46			79.13	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
996	1f2q	A	58	225	9.8e-36			140.65	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI- ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
996	1f6a	A	56	225	4.2e-36			141.95	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FCEPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
996	1fcg	A	55	224	1.4e-36			135.32	CHAIN C REGION; FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
996	1fhl	A	54	229	7e-34			127.96	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
996	1qnx	A	1	180	9.8e-46			89.64	VES V 5; CHAIN: A;	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
996	2fcb	A	55	226	2.8e-38			135.92	FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
999	1byg	A	1	271	1.3e-59			81.76	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
999	1e3h	A	2	476	1.4e-87			148.05	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP 2 DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
999	1e3h	A	9	474	1.4e-87	0.11	-1202.08		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
999	1e3p	A	2	476	1.4e-87			140.99	GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	DIPHOSPHOTRANSFERASE, RNA PROCESSING, RNA DEGRADATION
										POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION
999	1e3p	A	9	474	1.4e-87	0.17	-1202.08		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION
										TRANSFERSCRIPTION INHIBITOR BETA-PROPELLER
999	1ej	A	12	344	2.8e-39			82.19	TRANSFERSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
999	1fgk	A	4	271	1.3e-55			101.99	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE,
999	1fgk	B	2	271	2.8e-56			99.67	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
999	1got	B	5	343	2.8e-51			75.43	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
999	1lep	A	1	271	5.6e-74			115.77	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
999	1it3	A	1	271	1.3e-55			90.03	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
999	1qpc	A	3	270	9.8e-77			105.38	LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1000	1a1n	A	17	117	9.8e-45	0.69	-1202.08		B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1000	1aga	B	22	115	2.8e-39	0.54	-1202.08		HLA-DR3; CHAIN: A, B; CLIP; CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN) MHC GLYCOPROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1000	1agd	A	17	117	4.2e-44	0.36	-1202.08		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE); CHAIN: C;	COMPLEX (TRANSMEMBRANE/GLYCOPROTEIN)
1000	1agd	B	22	115	2.8e-39	0.78	-1202.08		HLA-DRI CLASS II HISTOCOMPATIBILITY PROTEIN; CHAIN: A, B, D, E, G, H, J, K; HLA-A2; CHAIN: C, F, I, L;	COMPLEX (MHC PROTEIN/ANTIGEN) DRA, DRB1 01010; COMPLEX (MHC PROTEIN/ANTIGEN), HISTOCOMPATIBILITY ANTIGEN
1000	1efx	A	17	118	1.4e-44	0.54	-1202.08		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1000	1fzk	B	1	85	7e-32			129.28	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC
1000	1fzk	B	21	119	1.4e-35			166.40	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN:	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	
1000	1hsa	A	17	117	9.8e-45	0.39	-1202.08		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1000	1i4f	A	17	116	8.4e-42	0.46	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGF-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1000	1jk8	B	22	115	2.8e-40	0.24	-1202.08		MHC CLASS II HLA-DQ8; CHAIN: A; MHC CLASS II HLA-DQ8; CHAIN: B; INSULIN B PEPTIDE; CHAIN: C;	IMMUNE SYSTEM HLA-DQ8, INSULIN B PEPTIDE, TYPE 1 DIABETES, AUTOIMMUNITY
1000	1mhe	A	17	115	8.4e-40	0.60	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMARFVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1000	1qgd	A	17	115	1.3e-42	0.65	-1202.08		HISTOCOMPATIBILITY	IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1000	3ftu	B	1	85	5.6e-32			120.95	LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1000	3ftu	B	1	85	5.6e-32			120.95	NEONATAL FC RECEPTOR; CHAIN: A, C, E; BETA-2-MICROGLOBULIN; CHAIN: B, D, F;	FCRN, BRAMBELL RECEPTOR; COMPLEX (IMMUNOGLOBULIN/BINDING PROTEIN)
1000	3ftu	B	21	119	1.4e-35			157.46	NEONATAL FC RECEPTOR; CHAIN: A, C, E; BETA-2-MICROGLOBULIN; CHAIN: B, D, F;	FCRN, BRAMBELL RECEPTOR; COMPLEX (IMMUNOGLOBULIN/BINDING PROTEIN)
1007	1a7i		390	443	5.1e-15	0.43	0.58		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1007	1a7i		390	447	5.6e-10	0.17	0.66		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1007	1a7i		448	507	5.6e-14	-0.10	0.57		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1007	1a7i		449	506	1.7e-16	0.08	0.58		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1007	1a7i		510	575	3.4e-12	-0.05	0.30		QCRP2 (LIM1); CHAIN: NULL;	BINDING PROTEIN, ZINC 2 FINGER
1007	1a7i		510	577	9.8e-10	0.38	0.76		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1007	1b8t	A	383	572	1.2e-33	-0.26	0.03		CRP1; CHAIN: A;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1007	1b8t	A	449	577	8.4e-26	0.06	0.07		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1007	1c4l		382	443	1.7e-16	-0.38	0.33		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1007	1c4l		382	449	2.8e-13	-0.54	0.18		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1c4l		446	502	6.8e-14	-0.12	0.51		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1c4l		450	516	7e-16	-0.26	0.05		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1c4l		508	572	1.5e-13	-0.11	0.48		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1007	1ct1		510	577	2.8e-12	0.16	0.55		AVIAN CYSTEINE RICH PROTEIN; ICTL 3	ICTL 15 METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS
1007	1cxx	A	388	443	8.5e-16	0.52	0.68		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1cxx	A	388	446	4.2e-12	0.26	0.19		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1cxx	A	448	504	1.4e-14	0.45	0.78		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1cxx	A	507	572	8.5e-14	-0.05	0.25		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1cxx	A	507	574	9.8e-12	-0.37	0.89		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1007	1g47	A	381	450	2.8e-14	0.05	0.00		PINCH PROTEIN; CHAIN: A;	CELL ADHESION PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN; LIM DOMAIN; ZN FINGER
1007	1g47	A	510	577	1.4e-07	0.53	-0.09		PINCH PROTEIN; CHAIN: A;	CELL ADHESION PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN; LIM DOMAIN; ZN FINGER
1007	1im1		388	449	5.6e-12	0.37	0.57		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1im1		390	461	3.4e-16	-0.02	0.57		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1im1		449	512	1.4e-14	0.24	0.00		CYSTEINE RICH	METAL-BINDING PROTEIN CRIP;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQCOL D score	Compound	PDB annotation
									INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1iml		449	513	5.1e-16	0.01	0.47		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1iml		508	577	5.6e-12	0.07	1.00		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1007	1zfo		508	541	0.00056	-0.34	0.15		LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL- BINDING PROTEIN
1012	1a88	A	2	149	4.2e-27	0.54	0.00		CHLOROPEPOXIDASE L; CHAIN: A, B, C;	HALOPEPOXIDASE BROMOPEPOXIDASE L, HALOPEPOXIDASE L; HALOPEPOXIDASE, OXIDOREDUCTASE
1012	1a8q		2	156	4.2e-24	0.36	-0.07		BROMOPEPOXIDASE A1; CHAIN: NULL;	HALOPEPOXIDASE CHLOROPEPOXIDASE A1, HALOPEPOXIDASE A1; HALOPEPOXIDASE, OXIDOREDUCTASE
1012	1a8s		2	149	1.4e-26	0.53	0.39		CHLOROPEPOXIDASE F; CHAIN: NULL;	HALOPEPOXIDASE HALOPEPOXIDASE F; HALOPEPOXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX
1012	1aao	A	13	213	1.4e-24	0.45	1.00		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1012	1aao	A	13	229	1.8e-43	0.70	1.00		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1012	1aao	A	13	229	5.1e-31	0.53	1.00		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1012	1aao	A	8	214	1.4e-24			106.42	CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1012	1aao	A	8	230	1.8e-43			123.46	CARBOXYL ESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1012	1b6g		6	192	7e-19	0.02	0.09		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1012	1bn6	A	6	146	5.6e-22	0.18	0.62		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE DEHALOGENASE, ALPHA/BETA-HYDROLASE, DHIA, CRYSTAL STRUCTURE
1012	1c4x	A	9	157	8.4e-21	0.44	0.62		2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD: HYDROLASE, PCB DEGRADATION
1012	1c7j	A	7	198	3.4e-31	0.24	-0.07		PARA-NITROBENZYL ESTERASE; CHAIN: A;	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE, DIRECTED EVOLUTION, ORGANIC ACTIVITY, 2 PNB ESTERASE
1012	1cv2	A	12	144	2.8e-15	0.24	-0.05		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6-TETRACHLORO-1,4-CYCLOHEXADIENE DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
1012	1cvl		18	128	5.6e-09	0.60	0.19		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL-HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
1012	1din		5	199	7e-27	0.59	0.94		DIENELACTONE HYDROLASE; CHAIN: NULL;	HYDROLYTIC ENZYME DLH; DIENELACTONE HYDROLASE, AROMATIC HYDROCARBON CATABOLISM, 2 SERINE ESTERASE,

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
1012	1dqv	A	96	215	0.00034	0.31	0.71		ANTIGEN 85-C ₃ CHAIN: A, B;	CARBOXYMETHYLENEBUTENOLIDE, 3 HYDROLYTIC ENZYME IMMUNE SYSTEM 85C ANTIGEN, 85C, MYCOBACTERIUM TUBERCULOSIS, FIBRONECTIN
1012	1eas	A	3	223	1.7e-36	0.22	0.37		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
1012	1ehy	A	13	172	1.4e-20	0.53	0.16		SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN
1012	1ek1	A	2	149	2.8e-25	0.51	0.48		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1012	1ek1	B	2	149	2.8e-25	0.64	0.55		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1012	1eth	A	25	167	0.00014	0.52	0.03		TRIACYLGLYCEROL ACYL-HYDROLASE; CHAIN: A, C ₃ COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1012	1f6w	A	2	222	5.1e-34	0.33	-0.08		BILE SALT ACTIVATED LIPASE; CHAIN: A;	HYDROLASE BILE SALT ACTIVATED LIPASE, ESTERASE, CATALYTIC DOMAIN
1012	1f52	A	13	214	7e-32	0.84	1.00		ACYL PROTEIN THIOESTERASE 1; CHAIN: A, B;	HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1012	1fj2	A	13	231	3.4e-38	0.52	1.00		ACYL PROTEIN THIOESTERASE 1; CHAIN: A, B;	2 DIFFRACTION HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS 2 DIFFRACTION
1012	1fj2	A	1	215	7e-32			116.80	ACYL PROTEIN THIOESTERASE 1; CHAIN: A, B;	HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS 2 DIFFRACTION
1012	1gpl		25	167	0.00014	0.39	0.11		RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE, SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC HYDROLASE
1012	1i6w	A	23	166	8.4e-09	0.19	0.21		LIPASE A; CHAIN: A, B;	HYDROLASE ALPHA/BETA
1012	1jkm	A	5	157	7e-12	0.39	0.00		BREFELDIN A ESTERASE; CHAIN: A, B;	SERINE HYDROLASE SERINE HYDROLASE, DEGRADATION OF BREFELDIN A, ALPHA/BETA 2 HYDROLASE FAMILY
1012	1lpb	B	25	167	5.6e-05	0.25	0.04		HYDROLASE/CARBOXY LIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED 1LPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	
1012	1maa	A	3	221	5.1e-36	0.30	0.46		ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, Tetramer, 2 HYDROLASE FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1012	1qe3	A	7	198	3.4e-31	0.09	-0.07		PARA-NITROBENZYL ESTERASE; CHAIN: A;	GLYCOSYLATED PROTEIN HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE DIRECTED EVOLUTION
1012	1qge	D	18	128	5.6e-09	0.46	0.30		TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	HYDROLASE PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1012	1qj4	A	25	159	5.6e-09	0.23	-0.05		HYDROXYNITRILE LYASE; CHAIN: A;	LYASE OXYNITRILE LYASE; OXYNITRILE, CYANOGENESIS, CYANHYDRIN FORMATION, LYASE
1012	1qtr	A	1	130	2.8e-13	0.32	-0.02		PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1012	1thg		3	204	8.5e-30	0.05	0.07		HYDROLASE(CARBOXY LIC ESTERASE) LIPASE (E.C.3.1.1.3) TRIACYLGLYCEROL HYDROLASE 1THG 3	
1012	2bce		2	216	3.4e-35	0.32	-0.08		CHOLESTEROL ESTERASE; CHAIN: NULL;	HYDROLASE BILE SALT ACTIVATED LIPASE, BILE SALT STIMULATED HYDROLASE, SERINE ESTERASE, LIPASE
1012	4lip	D	18	128	1.4e-09	0.35	0.13		TRIACYL-GLYCEROL-HYDROLASE; CHAIN: D, E;	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
1017	1alh	A	211	293	1.2e-24	-0.05	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1alh	A	239	319	2.8e-29	-0.41	1.00		DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	239	348	5.1e-23	-0.37	0.51		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	463	543	3.4e-42	0.10	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	58	140	1.4e-25			77.51	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	72	154	1.4e-27			54.94	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	87	154	2.8e-31			57.17	QGSR ZINC FINGER	COMPLEX (ZINC FINGER/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE; CHAIN: A; DUPELEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1alh	A	90	169	1.1e-23	-0.34	0.00		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPELEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1017	1mey	C	116	198	2.8e-39	-0.24	0.17		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	172	263	7e-43	-0.07	0.92		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	210	291	9.8e-47	-0.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	238	319	2.8e-47	-0.33	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mey	C	266	347	8.4e-48	-0.03	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
1017	Imey	C	294	375	1.3e-48	0.16	0.98		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	29	111	2.8e-50			98.30	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	322	403	8.4e-50	0.63	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	350	431	2.8e-50	0.22	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	378	459	7e-51	0.23	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	406	487	5.6e-50	0.27	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	434	515	1.1e-49	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: C, F, G;	2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	462	543	4.2e-50	0.16	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	462	544	4.2e-50			102.09	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	490	565	1.4e-43	0.07	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	57	139	2.8e-50			100.99	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	71	153	2.8e-50			69.61	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	86	154	4.2e-50			76.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	Imey	C	88	169	1.4e-37	-0.48	0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
									FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mev	G	114	141	1.4e-09	-0.61	0.01		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mev	G	208	235	2.8e-11	0.29	0.63		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1mev	G	264	291	4.2e-12	-0.13	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1017	1ff3	A	173	259	4.2e-17	-0.08	0.11		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1017	1ff6	A	147	403	1.4e-49	-0.57	0.03		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1ff6	A	173	328	2.8e-34	-0.35	0.04		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1tt6	A	1	153	1.4e-36			90.49	CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	211	431	3.4e-55	-0.47	0.21		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	267	412	4.2e-38	0.01	0.90		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	2	153	4.2e-37			91.96	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	323	487	3.4e-68	-0.14	0.76		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	350	520	6.8e-72			108.86	TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
									TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	351	496	2.8e-39	0.13	1.00		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
									TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	379	543	6.8e-72	-0.19	1.00		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
									TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	407	551	2.8e-38	-0.00	0.99		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
									TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	435	565	1.4e-32	0.08	1.00		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1tt6	A	7	154	8.4e-37			68.08	CHAIN: B, C, E, F; TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	89	249	8.4e-31	0.13	0.24		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1017	1tt6	A	124	235	1.4e-27	-0.45	0.07		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	180	291	2.8e-30	-0.19	0.80		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	Iubd	C	1	111	2.8e-35			89.38	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	Iubd	C	237	375	3.4e-36	-0.42	0.81		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	Iubd	C	246	347	9.8e-34	-0.24	0.90		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	Iubd	C	265	403	3.4e-47	-0.33	0.62		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	Iubd	C	33	140	4.2e-36			66.22	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1ubd	C	348	460	6.8e-53	-0.08	1.00		DNA; CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	3	111	1.4e-36			82.90	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	433	544	1.7e-51	0.11	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	439	543	4.2e-35	0.01	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	1ubd	C	467	563	3.4e-45	0.02	0.83		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	1ubd	C	470	566	2.8e-32	0.17	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1017	2adr		177	238	3.4e-12	-0.04	0.19		ADRI; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR
1017	2gli	A	144	293	5.6e-30	-0.33	0.24		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	177	405	1.5e-51	-0.61	0.43		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	1	139	9.8e-34			85.51	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	1	140	2.8e-33			88.47	ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING PROTEIN/DNA)

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SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GLI1; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	238	377	1.3e-33	0.18	0.95		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	266	433	3.4e-61	0.07	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	2	141	2.8e-33			59.85	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	330	458	2.8e-35	0.16	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	350	489	1.2e-66	0.19	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	378	544	1e-67	0.13	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	414	545	4.2e-35	0.00	0.99		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gli	A	442	566	8.4e-33	-0.02	0.87		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1017	2gi	A	462	563	1.7e-45	0.30	0.78		ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	(DNA-BINDING PROTEIN/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1017	2gi	A	5	154	7e-32			62.95	ZINC FINGER PROTEIN GLI; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1020	1a7i		137	194	1.7e-16	0.13	0.99		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1020	1a7i		258	313	5.1e-10	0.37	0.66		QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1020	1a7i		9	69	5.6e-13			51.43	QCRP2 (LIM1); CHAIN: NULL;	LIM DOMAIN CONTAINING PROTEINS LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN, ZINC 2 FINGER
1020	1b8t	A	138	313	5.1e-29	-0.43	0.15		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1020	1b8t	A	199	313	2.8e-11	-0.05	0.28		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1020	1b8t	A	74	273	1.7e-37			102.41	CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1020	1b8t	A	76	251	1.7e-37	-0.51	0.57		CRP1; CHAIN: A;	DIFFERENTIATION, CONTRACTILE
1020	1c1l		136	192	1.7e-14	0.19	0.94		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1020	1c1l		1	79	2.8e-18			50.28	AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1020	1c1l		258	313	3.4e-10	0.69	0.51		AVIAN CYSTEINE RICH PROTEIN; 1CTL 3	METAL-BINDING PROTEIN LIM DOMAIN CONTAINING PROTEINS 1CTL 15
1020	1cxx	A	136	194	8.5e-15	0.41	0.81		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1020	1cxx	A	256	313	1.2e-11	0.71	0.99		CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1020	1cxx	A	8	67	1.3e-16			53.17	CYSTEINE AND GLYCINE-RICH PROTEIN CRP2; CHAIN: A;	SIGNALING PROTEIN LIM DOMAIN CONTAINING PROTEINS, METAL-BINDING PROTEIN
1020	1cxt	A	46	210	2.8e-07			62.37	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN
1020	1g44	C	31	290	0.0068			77.40	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1020	1iml		138	203	5.1e-15	0.20	0.18		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1020	1klo		14	182	6.8e-07			69.70	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1020	Imey	C	221	307	5.6e-36	0.03	-0.15		DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	1alh	A	350	432	3e-28			78.62	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1024	Imey	C	17	93	1.1e-46			61.77	DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	181	262	1.1e-47	0.11	-1202.08		DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	209	290	4.2e-49	0.23	-1202.08		DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	21	103	1.4e-50			99.15	DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	237	318	1.1e-49	0.70	-1202.08		DNA; CHAIN: A, B, D, E, CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1024	Imey	C	293	374	1.4e-50	0.14	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	29	111	1.4e-50			97.98	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	321	402	1.4e-50	0.32	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	349	430	1.4e-50	0.03	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	349	431	1.4e-50			100.76	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	377	438	5.6e-38	0.06	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1024	Imey	C	3	64	7e-40			59.08	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1024	1tt6	A	1	133	7e-34			64.03	CHAIN: C, F, G; TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1024	1tt6	A	1	144	1.4e-35			95.70	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1024	1tt6	A	265	430	1.5e-70			116.54	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1024	1tt6	C	181	291	3e-52			83.93	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1tt6	C	189	290	1.4e-35	0.16	-1202.08		YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1024	1ubd	C	1	111	2.8e-36			83.50	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1ubd	C	217	318	2.8e-35	0.16	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1ubd	C	21	131	1.4e-36			84.44	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1024	1ubd	C	235	346	3e-52	0.23	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1024	2gli	A	153	292	2.8e-33	0.01	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	REGULATION/DNA) COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	1	132	1.4e-32			87.11	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	1	133	8.4e-32			86.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	209	348	3e-66	0.17	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	217	345	4.2e-35	0.24	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	237	376	1.3e-67			98.02	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1024	2gli	A	301	429	7e-35	0.01	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1026	1dix	A	1	222	1.5e-05			51.64	SUBSTRATE BINDING DOMAIN OF DNAK; CHAIN: A; SUBSTRATE PEPTIDE (7 RESIDUES); CHAIN: B;	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE) DNAK, HEAT SHOCK PROTEIN 70 KDA (HSP70), COMPLEX 2 (MOLECULAR

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1026	1dky	B	1	206	0.0001			50.66	DNAK; CHAIN: A, B; PEPTIDE SUBSTRATE; CHAIN: C, D;	CHAPERONE/PEPTIDE) COMPLEX (MOLECULAR CHAPERONE/PEPTIDE) DNAK, HEAT SHOCK PROTEIN 70 KDA (HSP70), COMPLEX 2 (MOLECULAR CHAPERONE/PEPTIDE)
1029	1aut	L	261	326	0.00024	0.03	0.33		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1029	1dva	L	261	326	0.0006	-0.18	0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1029	1eis	A	115	200	7.2e-09	-0.02	0.11		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1029	1eis	A	196	270	6e-05	0.15	0.07		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1029	1ext	A	65	227	3e-27	0.00	-1202.08		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1029	1ext	A	98	249	2.4e-14			63.01	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1029	1g40	A	26	268	3e-29			93.82	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
1029	1g44	A	36	268	3e-28			93.40	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1029	1g44	B	42	268	6e-33			90.73	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1029	1g44	C	42	277	9e-24			92.61	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1029	1k1o		22	216	3e-14	0.04	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1029	1k1o		27	190	3e-14			71.49	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1029	1pfx	L	10	144	2.4e-13			64.18	FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR, COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1029	1qub	A	7	275	3e-30			68.14	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1029	9wga	A	93	269	1.5e-30			94.61	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1031	1awq	A	2	164	2.8e-91	1.33	-1202.08		(ISOLECTIN 2) 9WGA 3	
									CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
1031	1awq	A	2	165	2.8e-91			269.60	CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
1031	1ctq	A	7	178	2.8e-63			98.08	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1035	1alh	A	13	99	2.8e-29			77.80	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1035	1alh	A	98	182	8.4e-23	0.31	-1202.08		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1035	1mey	C	129	210	2.8e-41	0.38	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1mey	C	12	94	9.8e-51			95.25	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	12	98	4.2e-49			94.62	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	157	238	4.2e-44	0.20	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	185	266	2.8e-46	0.09	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	1	67	1.4e-41			73.50	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	213	294	4.2e-48	0.10	-1202.08		DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	23	105	9.8e-51			96.53	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	269	350	1.4e-48	0.12	-1202.08		DNA: CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	297	378	2.8e-49	0.50	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	325	406	7e-50	0.16	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	353	434	7e-50	0.49	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	381	462	2.8e-50	0.27	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	409	490	5.6e-51	0.51	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	437	518	1.4e-50	0.28	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1035	Imey	C	465	546	1.3e-50	0.23	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	493	574	8.4e-50	0.03	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	49	131	1.4e-50			89.69	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	6	85	7e-50			90.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	97	182	9.8e-38	0.42	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	Imey	C	98	182	3e-38	0.45	-1202.08		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1035	1tf3	A	12	101	4.2e-14			58.28	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIA; 5S GENE; NMR, TFIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1035	1tt6	A	1	134	8.4e-36			71.45	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1tt6	A	1	145	1.4e-35			84.26	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1tt6	A	242	387	5.6e-38	0.02	-1202.08		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1tt6	A	381	544	4.5e-69			113.05	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1tt6	A	410	556	9.8e-39	0.16	-1202.08		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1tt6	A	438	574	1.4e-37	0.07	-1202.08		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1tt6	A	439	574	1e-53	0.16	-1202.08		TFIIIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1035	1ubd	C	100	210	4.2e-27	0.01	-1202.08		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	12	106	1.4e-29			68.31	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	1	103	4.2e-36			76.28	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									INITIATOR ELEMENT DNA; CHAIN: A, B;	1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	23	133	4.2e-36			83.22	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	323	434	4.5e-49	0.40	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	358	462	1.4e-36	0.04	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	417	518	1.4e-36	0.02	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
1035	1ubd	C	435	546	6e-51	0.41	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	463	574	1.5e-49	-0.00	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	1ubd	C	67	182	1.5e-37	0.45	-1202.08		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1035	2gli	A	1	110	1.3e-25			53.64	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	1	132	4.2e-33			76.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1035	2gli	A	1	134	2.8e-33			82.37	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	297	436	4.5e-65			98.88	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	297	492	4.5e-65	0.00	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	333	461	7e-35	0.54	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	333	520	7.5e-64	0.04	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	389	520	2.8e-35	0.13	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	417	545	8.4e-35	0.19	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	439	574	1.2e-61	0.16	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1035	2gli	A	69	212	1.1e-26	0.07	-1202.08		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1042	12e8	H	336	518	5.6e-51	-0.05	0.10		CHAIN: C, D; 2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1042	1a31	H	336	515	4.2e-50	0.02	0.19		IMMUNOGLOBULIN FAB 13G5; CHAIN: L, H;	IMMUNOGLOBULIN
1042	1adq	L	51	240	8.4e-32	-0.11	0.18		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1042	1afv	H	336	517	5.6e-51	0.17	0.10		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1042	1b1h	A	149	506	2.8e-27	0.13	0.87		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1042	1b1h	A	150	515	8.5e-45	0.37	0.80		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1042	1b1h	A	46	417	3.4e-48			130.68	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1042	1b1h	A	50	417	3.4e-48	0.15	1.00		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1bm3	H	336	519	1.3e-50	0.14	0.09		IMMUNOGLOBULIN OPG2 FAB, CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OPG2 FAB, VARIABLE DOMAIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN
1042	1c5c	H	336	519	2.8e-51	0.10	0.06		CHIMERIC DECARBOXYLASE ANTIBODY 21D8; CHAIN: L; CHIMERIC DECARBOXYLASE ANTIBODY 21D8; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN, CATALYTIC ANTIBODY, CHIMERIC FAB, 2 DECARBOXYLASE, HAPTEN COMPLEX
1042	1e1c	B	336	515	5.6e-51	-0.00	-0.02		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE
1042	1e1c	B	48	244	2.8e-72	0.16	-0.06		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE
1042	1e17	I	434	519	7e-25	0.08	0.09		IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696	IMMUNE SYSTEM IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEASE, ENZYME 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1cql	A	418	516	1.4e-25	0.23	-0.11		(CONSTANT HEAVY CHAIN); CHAIN: I;	INHIBITION, IMMUNOGLOBULIN
									CH3 DOMAIN OF MAK33 ANTIBODY; CHAIN: A, B;	IMMUNE SYSTEM CONSTANT DOMAIN, C1-SUBSET, IMMUNOGLOBULIN, IMMUNE SYSTEM
1042	1cs6	A	135	515	3.4e-46	0.31	0.62		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1cs6	A	149	517	1.4e-35	0.19	0.77		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1cs6	A	244	602	1.1e-34	0.11	0.46		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1cs6	A	43	418	1.7e-56			125.44	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1cs6	A	50	416	1.7e-56	-0.10	0.71		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1042	1dgi	R	151	416	5.1e-28	-0.23	0.47		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1042	1dgi	R	49	331	3.4e-43			112.84	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1042	1dgi	R	52	331	3.4e-43	-0.28	0.05		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1dn2	A	250	415	1.3e-35	-0.05	0.07		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1042	1e4k	A	244	415	1.4e-36	-0.26	0.06		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
1042	1e4x	H	336	518	4.2e-51	0.32	0.27		TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
1042	1e4x	H	48	247	1.4e-74	0.08	-0.11		TAB2; CHAIN: L, M; TAB2; CHAIN: H, I; CYCLIC PEPTIDE; CHAIN: P, Q	COMPLEX (ANTIBODY/ANTIGEN) CROSS-REACTIVITY, PROTEIN-PEPTIDE RECOGNITION
1042	1eap	B	49	241	1.1e-65	-0.06	0.29		CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] LEAP 3 PHOSPHONATE LEAP 4	
1042	1ejo	H	51	244	1.1e-65	0.05	0.00		IGG2A MONOCLONAL ANTIBODY (LIGHT CHAIN); CHAIN: L; IGG2A MONOCLONAL ANTIBODY (HEAVY CHAIN); CHAIN: H; FMDV PEPTIDE; CHAIN:	IMMUNE SYSTEM FMDV, ANTIGENIC-ANTIBODY INTERACTIONS, RGD MOTIF, G-H LOOP 2 OF VP1.

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1evt	C	247	416	8.5e-27	0.27	0.88		P ₁ FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1042	1f2q	A	250	420	1.2e-26	0.13	0.87		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1042	1f6a	A	246	420	5.1e-31	0.06	0.72		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1042	1fai	H	48	241	8.4e-68	0.07	-0.05		IMMUNOGLOBULIN FAB FRAGMENT FROM A MONOCLONAL ANTILARSONATE ANTIBODY, R19.9 IFAI 3 (IGG2B,KAPPA) IFAI 4	
1042	1fbi	H	48	244	1.1e-72	0.05	-0.17		COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY P9.13.7 (IGG1) IFBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) IFBI 4	
1042	1fc2	D	250	415	7e-36	0.07	0.06		IMMUNOGLOBULIN IMMUNOGLOBULIN FC	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
1042	1fgn	H	337	514	7e-51	0.11	0.48		IMMUNOGLOBULIN FAB 5G9; CHAIN: L, H;	IMMUNOGLOBULIN FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN; ANTIBODY, FAB, ANTI-TF, MONOCLONAL, MURINE, IMMUNOGLOBULIN
1042	1fh5	H	54	244	8.4e-66	0.14	0.07		MONOCLONAL ANTIBODY MAK33; CHAIN: L; MONOCLONAL ANTIBODY MAK33; CHAIN: H;	IMMUNE SYSTEM FAB, BIP, CRYSTAL STRUCTURE
1042	1f3	A	51	243	7e-66	-0.02	0.06		BLUE FLUORESCENT ANTIBODY (19G2)-HEAVY CHAIN; CHAIN: H, A; BLUE FLUORESCENT ANTIBODY (19G2)-LIGHT CHAIN; CHAIN: L, B;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1042	1for	H	50	244	4.2e-72	0.03	-0.06		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB17-1A) (ORTHORHOMBIC CRYSTAL FORM) 1FOR 3	
1042	1fsk	C	336	519	1.4e-50	0.11	0.01		MAJOR POLLEN ALLERGEN BET V 1-A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F;	IMMUNE SYSTEM BET V 1-A, BETVI ALLERGEN, BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V 1, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1fsk	C	48	244	2.8e-72	0.05	-0.14		L ₁ , MAJOR POLLEN ALLERGEN BET V I-A; CHAIN: A, D, G, J; IMMUNOGLOBULIN KAPPA LIGHT CHAIN; CHAIN: B, E, H, K; ANTIBODY HEAVY CHAIN FAB; CHAIN: C, F, I, L ₂	IMMUNE SYSTEM BET V I-A, BETVI ALLERGEN; BV16 FAB-FRAGMENT, KAPPA MOPC21 CODING SEQUENCE; HEAVY CHAIN OF THE MONOCLONAL ANTIBODY MST2; BET V I, BV16 FAB FRAGMENT, ANTIBODY ALLERGEN COMPLEX
1042	1hi6	B	50	246	1.1e-70	0.29	0.22		IGG2A KAPPA ANTIBODY CB41 (LIGHT CHAIN); CHAIN: A; IGG2A KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M ₂	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSSREACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1
1042	1hzh	H	163	521	4.2e-63	0.12	0.55		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M ₂	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
1042	1hzh	H	48	418	0	0.28	0.55		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M ₂	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
1042	1hzh	H	4	320	1.4e-51	-0.22	0.81		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M ₂	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQROL D score	Compound	PDB annotation
1042	1ile	A	251	415	7e-30	0.07	-0.11		IG GAMMA-2A CHAIN C REGION; CHAIN: A, B;	IMMUNE SYSTEM IGG2A, IGG, FC
1042	1ibg	H	49	241	5.6e-67	0.10	0.13		IMMUNOGLOBULIN IGG FAB (IGG2B, KAPPA) FRAGMENT (40-50 FAB) COMPLEXED WITH IIBG 3 OUBABAIN IIBG 4	
1042	1igt	B	160	517	9.8e-61	-0.03	0.54		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1042	1igt	B	49	415	0	0.10	0.66		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1042	1igt	B	51	475	0			102.57	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1042	1igt	B	5	318	2.8e-48	-0.12	0.28		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1042	1igy	B	160	516	5.6e-61	0.04	0.64		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1042	1igy	B	49	415	0	-0.03	0.31		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1042	1il1	A	50	244	7e-68	0.06	-0.02		MONOCLONAL ANTIBODY G3-519 (HEAVY CHAIN); CHAIN: A; MONOCLONAL ANTIBODY G3-519 (LIGHT CHAIN); CHAIN: B;	IMMUNE SYSTEM FAB, BETA SHEET STRUCTURE, ANTIBODY
1042	1ibb	B	261	517	1e-36	0.15	0.71		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1	COMPLEX (IMMUNOGLOBULIN/RECEPTOR)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									INTERLEUKIN-1 RECEPTOR, CHAIN: B;	IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1042	1kb5	H	49	244	2.8e-72	0.10	0.06		KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPLHA VBETA DOMAIN; T-CELL RECEPTOR, STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
1042	1mco	H	189	516	1.1e-67	0.05	0.01		IMMUNOGLOBULIN	
									IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1042	1mco	H	48	415	0	0.05	0.66		IMMUNOGLOBULIN	
									IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1042	1mco	H	49	475	0			106.26	IMMUNOGLOBULIN	
									IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1042	1mco	H	5	320	2.8e-55	-0.30	0.09		IMMUNOGLOBULIN	
									IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1042	1mcp	H	49	231	1.1e-48	-0.07	0.11		IMMUNOGLOBULIN	
									IMMUNOGLOBULIN FAB FRAGMENT (MC/PC\$603)	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1mlb	B	336	519	1.4e-50	0.16	0.07		IMCP 4 IMMUNOGLOBULIN FAB D44.1 (GG1,KAPPA) (BALB/C MOUSE, MONOCLONAL ANTIBODY) IMLB 5	
1042	1pfc		417	520	2.8e-23	0.02	-0.13		IMMUNOGLOBULIN SP/FC(PRIME) FRAGMENT OF AN IG*G1 IPEC 4	
1042	1plg	H	48	243	4.2e-73	0.17	-0.05		IGG2A-KAPPA=, IPLG 4 CHAIN: L, H; IPLG 5	IMMUNOGLOBULIN
1042	1psk	H	49	240	1.4e-61	-0.17	0.04		ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FAB, GD2-GANGLIOSIDE, CARBOHYDRATE, MELANOMA, IMMUNOGLOBULIN
1042	1qfu	H	336	518	1.3e-50	0.30	0.28		HEMAGGLUTININ (HA1 CHAIN); CHAIN: A; HEMAGGLUTININ (HA2 CHAIN); CHAIN: B; IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY (LIGHT CHAIN); CHAIN: L; IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY (HEAVY CHAIN); CHAIN: H;	VIRAL PROTEIN/IMMUNE SYSTEM COMPLEX (HEMAGGLUTININ/IMMUNOGL OBULIN), HEMAGGLUTININ, 2 IMMUNOGLOBULIN, VIRAL PROTEIN/IMMUNE SYSTEM
1042	1qfu	H	48	244	1.4e-72	0.10	-0.11		HEMAGGLUTININ (HA1 CHAIN); CHAIN: A; HEMAGGLUTININ (HA2 CHAIN); CHAIN: B; IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY (LIGHT CHAIN); CHAIN: L; IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY	VIRAL PROTEIN/IMMUNE SYSTEM COMPLEX (HEMAGGLUTININ/IMMUNOGL OBULIN), HEMAGGLUTININ, 2 IMMUNOGLOBULIN, VIRAL PROTEIN/IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1042	1vge	H	51	244	1.4e-66	-0.10	0.18		(HEAVY CHAIN), CHAIN: H; TR1.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TR1.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
1042	1wej	H	336	520	8.4e-51	0.24	0.27		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1042	1yej	H	50	244	8.4e-69	0.18	-0.01		IG ANTIBODY D2.3 (LIGHT CHAIN); CHAIN: L; IG ANTIBODY D2.3 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM ABZYME, TRANSITION STATE ANALOG, IMMUNE SYSTEM
1042	25c8	H	336	515	1.4e-51	0.11	0.16		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1042	2fbj	H	49	231	7e-51	-0.03	0.04		IMMUNOGLOBULIN IG* A FAB FRAGMENT (J539) (GALACTAN-BINDING) 2FBJ 3	
1042	2fcb	A	249	419	3.4e-28	0.11	0.74		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1042	3fct	B	336	518	4.2e-50	0.22	0.09		METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CATALYTIC ANTIBODY; CHAIN: B, D;	
1043	1cdq		88	164	8.4e-20	0.59	1.00		COMPLEMENT REGULATORY PROTEIN CD59 (NMR, 20 STRUCTURES) 1CDQ 3	
1043	1cdq		88	164	8.4e-20			142.11	COMPLEMENT REGULATORY PROTEIN CD59 (NMR, 20 STRUCTURES) 1CDQ 3	
1043	1etg		88	157	2.8e-19	0.41	1.00		COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN CD59 (EXTRACELLULAR 1ERG 3 REGION, RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	
1043	1etg		88	157	2.8e-19			131.94	COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN CD59 (EXTRACELLULAR 1ERG 3 REGION, RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	
1047	1ain	A	11	199	0			232.06	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1047	1aln	A	25	299	0			410.38	B*3501; CHAIN: A, B; PEPTIDE VPLRPMITY; CHAIN: C;	(ANTIGEN/PEPTIDE) COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1047	1aln	A	25	300	0	0.83	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMITY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1047	1agd	A	11	199	0			233.86	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1047	1agd	A	25	299	0			411.64	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1047	1agd	A	25	300	0	0.79	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1047	1etx	A	25	302	0	0.87	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1047	1efx	A	25	302	0			420.37	CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1047	1hsa	A	11	199	0			232.10	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1047	1hsa	A	25	299	0			410.78	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1047	1hsa	A	25	300	0	0.82	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B(ASTERISK)2705\$ 1HSA 4	
1047	1hsb	A	11	199	0			257.74	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1047	1hsb	A	25	294	0	0.86	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1047	1hsb	A	25	294	0			414.03	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1047	14f	A	11	199	1.4e-100			263.59	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGF-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUCOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1047	14f	A	25	299	0	0.83	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN	IMMUNE SYSTEM MAGF-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUCOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1047	1i4f	A	25	299	0			435.50	4; CHAIN: C; HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; MELANOMA- ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1047	1qgd	A	12	199	0			232.33	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1047	1qgd	A	26	298	0	0.87	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1047	1qgd	A	26	298	0			407.96	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1047	1tmc	A	11	185	2.8e-94			284.63	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1048	1efx	A	11	199	0			241.21	HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1048	2ebo	A	12	88	4.2e-18	-0.74	0.29		EBOLA VIRUS ENVELOPE GLYCOPROTEIN; CHAIN: A; GLYCOPROTEIN; CHAIN: A, B, C; T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	ENVELOPE GLYCOPROTEIN ENVELOPE GLYCOPROTEIN, FILOVIRUS, EBOLA VIRUS, GP2, COAT 2 PROTEIN
1050	1cdy		32	133	3.4e-07	0.40	0.19		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1050	1dgi	R	25	127	2.8e-29	0.41	0.46		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1050	1dt9	A	32	126	8.5e-10	0.33	0.06		T LYMPHOCYTE ACTIVATION ANTIGEN; CHAIN: A;	IMMUNE SYSTEM B7-1 (CD80); IG SUPERFAMILY
1050	1eaj	A	33	127	1.7e-07	0.41	-0.03		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
1050	1hxm	B	20	123	1.5e-06	0.36	0.06		GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C, E, G; GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T-CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GPCR
1050	1h8l	C	33	120	8.5e-06	0.12	0.80		T LYMPHOCYTE ACTIVATION ANTIGEN CD80; CHAIN: A, B; CYTOTOXIC T-LYMPHOCYTE PROTEIN 4; CHAIN: C, D;	IMMUNE SYSTEM ACTIVATION B7-1 ANTIGEN, CTLA-4 COUNTER-RECEPTOR CTLA-4, CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN RECEPTORS, INHIBITORY COMPLEX
1050	1h1l	G	32	131	7e-06	0.21	-0.03		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1050	1neu		27	128	6.8e-11	0.56	0.13		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, STRUCTURAL PROTEIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD, SIGNAL, MYELIN 2 MEMBRANE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1050	2cd0	A	29	127	8.4e-06	0.35	0.31		BENCE-JONES PROTEIN WIL, A VARIABLE DOMAIN FROM CHAIN: A, B;	ADHESION MOLECULE
1052	1tgc	A	55	98	0.0031	-0.49	0.01		CYTOTOXIN TOXIN GAMMA (CARDIOTOXIN) 1TGC 3	
1052	2crt		55	98	0.0023	-0.25	0.00		CARDIOTOXIN CARDIOTOXIN III (NMR, 13 STRUCTURES) 2CRS 3	
1054	1a5e		117	272	8.4e-20			74.90	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1054	1awc	B	95	244	7e-38			75.28	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1054	1bd8		93	247	4.2e-31			71.99	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1054	1bix	B	95	250	2.8e-31			71.23	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1054	1bu9	A	91	255	4.2e-33			80.55	CYCLIN-DEPENDENT	HORMONE/GROWTH FACTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1054	1by2		1	113	8.4e-44			114.47	KINASE 6 INHIBITOR; CHAIN: A;	P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1054	1by2								MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1054	1by2		711	824	7e-44			113.40	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1054	1by2		714	822	7e-44	0.79	1.00		MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1054	1ctu	A	217	709	1.4e-74			146.51	SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE BETA-PROPELLER, SUPERBARREL, COMPLEX WITH THE COFACTOR PQQ 2 AND THE INHIBITOR METHYLHYDRAZINE, OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1054	1ctu	A	218	645	1.4e-74	0.34	0.92		SOLUBLE QUINOPROTEIN GLUCOSE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE BETA-PROPELLER, SUPERBARREL, COMPLEX WITH THE COFACTOR PQQ 2 AND THE INHIBITOR METHYLHYDRAZINE, OXIDOREDUCTASE
1054	1d9s	A	2	129	2.8e-07			51.72	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1054	1hhb	A	96	246	4.2e-33			78.44	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1054	1lkn	D	95	296	2.8e-38			80.27	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C, I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1054	1myo		127	244	1.3e-26			72.80	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1054	1nfi	E	87	292	5.6e-38			75.42	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1057	1e9t	A	220	269	1.3e-11	0.15	-1202.08		INTESTINAL TREFOIL FACTOR; CHAIN: A;	CELL MOTILITY FACTOR HITF; INTESTINAL TREFOIL FACTOR, SOLUTION STRUCTURE, TREFOIL 2 DOMAIN, NMR SPECTROSCOPY, CELL MOTILITY FACTOR
1057	1ht7	A	222	275	7.5e-16	0.26	-1202.08		PS2 PROTEIN; CHAIN: A;	GROWTH FACTOR PNR-

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B ₂	2.PS2,TFE1,BREAST CANCER ESTROGEN INDUCIBLE GROWTH FACTOR, CELL MOTILITY, TUMOR SUPPRESSOR, TREFOIL 2 DOMAIN, SIGNAL
1057	2psp	A	223	269	1.5e-11	0.35	-1202.08		PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	TREFOIL FAMILY OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL
1063	1aln	A	29	255	0	0.27	-1202.08		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1063	1a6z	A	22	227	1.1e-68			53.05	HFE; CHAIN: A, C, BETA-2-MICROGLOBULIN; CHAIN: B, D	MHC CLASS I COMPLEX HFE, HEREDITARY HEMOCHROMATOSIS, MHC CLASS I
1063	1a6z	A	29	255	1.4e-68			59.25	HFE; CHAIN: A, C, BETA-2-MICROGLOBULIN; CHAIN: B, D	MHC CLASS I COMPLEX HFE, HEREDITARY HEMOCHROMATOSIS, MHC CLASS I
1063	1agd	A	29	255	0	0.36	-1202.08		B*0801; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1063	1c16	A	29	255	2.8e-67			50.68	MHC-LIKE PROTEIN T22; CHAIN: A, C, E, G; BETA-2-MICROGLOBULIN; CHAIN: B, D, F, H	IMMUNE SYSTEM NON-CLASSICAL MHC-LIKE, MAJOR HISTOCOMPATIBILITY, BETA2-2 MICROGLOBULIN
1063	1d2v	C	118	585	0			522.22	MYELOPEROXIDASE;	OXIDOREDUCTASE HEME-

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pos Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX
1063	1ed3	A	29	255	0	0.40	-1202.08		CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2- MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (13N3E); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1063	1ed3	A	29	255	0			58.49	CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2- MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (13N3E); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1063	1efx	A	29	255	0	0.44	-1202.08		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1063	1efx	A	29	255	0			57.25	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	FOLD, RECEPTOR/MHC COMPLEX
1063	1fzk	A	29	255	5.6e-98			58.77	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC
1063	1hoc	A	29	255	2.8e-98			50.16	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D=B=, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1063	1hsa	A	29	255	0	0.24	-1202.08		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1063	1hsb	A	29	255	0	0.40	-1202.08		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
1063	1hsb	A	29	255	0			52.66	(LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
									HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1063	1hyr	C	21	227	8.4e-55			52.26	NRG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C- TYPE-LECTIN LIKE, MIC-2 A, MHC-I, COMPLEX, IMMUNE SYSTEM
1063	1hyr	C	28	255	1.4e-53			67.13	NRG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D, MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C- TYPE-LECTIN LIKE, MIC-2 A, MHC-I, COMPLEX, IMMUNE SYSTEM
1063	1i4f	A	29	255	0	0.47	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1063	1i4f	A	29	255	0			60.36	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1063	1ld9	A	29	254	0			56.90	4; CHAIN: C; MHC CLASS I H-2LD HEAVY CHAIN; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; NANO- PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX LD; MAJOR HISTOCOMPATIBILITY COMPLEX, LD
1063	1ld9	A	29	255	0	0.20	-1202.08		MHC CLASS I H-2LD HEAVY CHAIN; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; NANO- PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX LD; MAJOR HISTOCOMPATIBILITY COMPLEX, LD
1063	1qo3	A	30	255	0	0.46	-1202.08		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1063	1qo3	A	30	255	0			54.24	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1063	1qpd	A	30	255	0	0.20	-1202.08		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1063	1qgd	A	30	255	0			53.86	MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1063	1tmc	A	22	192	9.8e-79			68.60	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1063	1zag	A	29	255	5.6e-62			55.36	ZINC-ALPHA-2-GLYCOPROTEIN; CHAIN: A, B, C, D;	LIPID MOBILIZATION FACTOR ZN-ALPHA-2-GLYCOPROTEIN, ZAG LIPID MOBILIZATION FACTOR, SECRETED MHC CLASS I HOMOLOG
1065	1eqj	A	71	336	4.2e-29	0.11	-1202.08		PHOSPHOGLYCERATE MUTASE; CHAIN: A;	ISOMERASE ALPHA/BETA-TYPE STRUCTURE
1066	12e8	H	2	227	8.4e-09			59.62	2B8 (GG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1066	1bih	A	29	376	1.1e-29			78.69	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1066	1b1h	A	30	346	1.1e-29	0.07	-1202.08		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1066	1cs6	A	20	376	2.8e-35			85.17	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1066	1cvs	D	122	302	7e-31	0.12	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1066	1cvs	D	37	208	2.8e-23	0.25	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1066	1dgi	R	12	303	9e-22			63.55	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PYR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1066	1ev2	G	132	308	4.2e-30	0.09	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1066	1ev1	C	37	208	2.8e-22	0.16	-1202.08		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1, FGFR1; IMMUNOGLOBULIN (IG) LIKE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR RECEPTOR 1; CHAIN: C, D;	DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IGL-LIKE DOMAINS, B-TREFOIL FOLD
1066	1f2q	A	121	308	8.4e-23	0.18	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1066	1f2q	A	26	214	4.2e-28			66.45	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1066	1f2q	A	28	214	4.2e-28	0.23	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1066	1f42	A	21	325	1.2e-08			63.76	INTERLEUKIN-12 BETA CHAIN; CHAIN: A;	CYTOKINE CYTOKINE
1066	1f6a	A	24	213	1.4e-29			75.69	HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1066	1f6a	A	24	214	1.4e-29	0.42	-1202.08		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1066	1f8t	H	2	227	4.2e-08			66.69	ANTIBODY FAB FRAGMENT (LIGHT	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: CHAIN: L; ANTIBODY FAB FRAGMENT (HEAVY CHAIN); CHAIN: H	FRAGMENT, INTERLEUKIN-2 2, X-RAY ANALYSIS, CRYSTAL
1066	1f97	A	101	309	1.4e-29			72.64	JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1066	1fcg	A	120	305	3e-23	0.14	-1202.08		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1066	1fcg	A	23	210	8.4e-28			78.62	FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1066	1fhl	A	117	307	1.5e-23	0.05	-1202.08		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1066	1fhl	A	22	211	7e-27			73.09	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1066	1fhl	A	28	212	7e-27	0.17	-1202.08		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1066	1g0x	A	118	310	2.8e-22			72.43	LEUCOCYTE IMMUNOGLOBULIN- LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUKOCYTE INHIBITORY RECEPTOR-1; LEUKOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1g0x	A	120	297	9e-22	0.18	-1202.08		LEUCOCYTE IMMUNOGLOBULIN- INHIBITORY RECEPTOR-1;	IMMUNE SYSTEM LEUKOCYTE INHIBITORY RECEPTOR-1;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									LIKE RECEPTOR-1; CHAIN: A;	LEUKOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1g0x	A	120	306	2.8e-22	0.21	-1202.08		LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUCOCYTE INHIBITORY RECEPTOR-1; LEUKOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1g0x	A	28	210	5.6e-26	0.21	-1202.08		LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUCOCYTE INHIBITORY RECEPTOR-1; LEUKOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1066	1igy	B	3	376	8.4e-09			65.38	IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1066	1mco	H	2	376	5.6e-10			74.55	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1066	1mkr		29	211	9.8e-26	0.21	-1202.08		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1066	1mkr		31	211	5.6e-33			71.40	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL, INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1066	2dli	A	119	304	2.8e-32	0.16	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1066	2dli	A	216	331	9.8e-09	0.06	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNOGLOBULIN
1066	2dli	A	29	210	1.1e-24	0.43	-1202.08		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1066	2dli	A	31	213	2.8e-32			74.62	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1066	2fcb	A	120	306	3e-23	0.14	-1202.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1066	2fcb	A	23	214	1.4e-29			81.15	FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1066	2fcb	A	24	213	1.4e-29	0.12	-1202.08		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1066	2nmb	A	1	141	5.6e-33			52.09	NLMB PROTEIN; CHAIN: A; GPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETRIC CELL DIVISION
1066	32c2	B	2	225	9.8e-09			60.00	IGG1 ANTIBODY 32C2; CHAIN: A; IGG1 ANTIBODY 32C2;	IMMUNE SYSTEM FAB, ANTIBODY, AROMATASE, P450

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1067	1bx2	A	8	64	2.8e-16			54.02	CHAIN: B; BST; CHAIN: A;	HYDROLASE INHIBITOR BOMBINA SKIN TRYPSIN INHIBITOR BETA-SHEET DISULFIDE-RICH
1069	1b6c	B	1	299	0			340.18	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1069	1b6c	B	253	586	0			351.53	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1069	1b6c	B	264	581	0	0.64	-1202.08		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1069	1es7	B	33	108	1.4e-12	0.14	-1202.08		BONE MORPHOGENETIC PROTEIN-2; CHAIN: A, C; BONE MORPHOGENETIC PROTEIN RECEPTOR 1A; CHAIN: B, D;	CYTOKINE BMP-2; ALK-3; PROTEIN-PROTEIN COMPLEX, THREE FINGER TOXIN FOLD, RECEPTOR-2 LIGAND COMPLEX, CYTOKINE RECEPTOR, TGF BETA SUPERFAMILY
1071	1aln	A	24	299	0			166.47	B*3501; CHAIN: A, B; PEPTIDE VPRLPMITY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1071	1aln	A	26	298	0	0.49	-1202.08		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1071	1agd	A	24	299	0			169.42	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1071	1agd	A	26	298	0	0.41	-1202.08		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL-INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1071	1c16	A	24	299	5.6e-89			139.27	MHC-LIKE PROTEIN T22; CHAIN: A, C, E, G; BETA-2-MICROGLOBULIN; CHAIN: B, D, F, H	IMMUNE SYSTEM NON-CLASSICAL MHC-LIKE, MAJOR HISTOCOMPATIBILITY, BETA2-2 MICROGLOBULIN
1071	1ed3	A	24	300	0			157.88	CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-B (13N3E); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1071	1ed3	A	26	298	0	0.52	-1202.08		CLASS I MAJOR	IMMUNE SYSTEM MAJOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (13N3E); CHAIN: C, F;	HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1071	1efx	A	24	300	0			163.46	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1071	1efx	A	26	298	0	0.64	-1202.08		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1071	1fzk	A	24	296	0			167.88	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1071	1hoc	A	24	295	0			172.82	PROTEIN, CHAIN: P; HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D==B==, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1071	1hsa	A	24	299	0			167.79	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1071	1hsa	A	26	298	0	0.49	-1202.08		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1071	1hsb	A	24	293	0			166.59	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1071	1hsb	A	26	293	0	0.46	-1202.08		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1071	1hyt	C	10	193	2.8e-53			236.94	ANTIGEN) IHSB 4 NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE-LECTIN LIKE, MIC-2 A, MIC-I, COMPLEX, IMMUNE SYSTEM
1071	1hyt	C	23	297	6e-93			439.85	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB11; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE-LECTIN LIKE, MIC-2 A, MIC-I, COMPLEX, IMMUNE SYSTEM
1071	1i4f	A	24	298	0			168.36	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1071	1i4f	A	26	298	0	0.49	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1071	1i49	A	24	291	0			166.41	MHC CLASS I H-2LD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NANO-PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX LD; MAJOR HISTOCOMPATIBILITY COMPLEX, LD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1071	1mhc	A	24	299	0			156.53	MHC CLASS I ANTIGEN H2-M3; 1MHC 6 CHAIN: A, B, D, E; 1MHC 7 NONAPEPTIDE FROM RAT NADH DEHYDROGENASE; 1MHC 12 CHAIN: C, F; 1MHC 13	HISTOCOMPATIBILITY ANTIGEN/PEPTIDE MAJOR HISTOCOMPATIBILITY COMPLEX; 1MHC 8 ND1; 1MHC 15
1071	1mhc	A	25	296	0			170.11	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1071	1mhc	A	26	297	0	0.53	-1202.08		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1071	1qo3	A	25	298	0			177.20	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
1071	1qo3	A	26	298	0	0.42	-1202.08		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1071	1qgd	A	25	296	0			173.19	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1071	1qgd	A	26	297	0	0.43	-1202.08		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1071	1tmc	A	11	185	8.4e-80			83.62	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1071	2fb4	H	212	305	1.1e-07	0.84	-1202.08		IMMUNOGLOBULIN	

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1071	2fgw	H	186	305	4.2e-08	0.18	-1202.08		IMMUNOGLOBULIN FAB 2FB4 4	
									FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY *H52* (HUH52-OZ FAB) 2FGW 4	
1087	1aox	A	356	548	4.2e-32	0.32	0.96		INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1087	1atz	A	358	516	4.2e-12	0.23	0.81		VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLOTIDE BINDING FOLD
1087	1auq		345	552	4.2e-54	0.16	0.16		AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1087	1ok4	A	361	545	1.4e-31	0.37	0.42		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
1087	1d2i	A	358	534	3.4e-14	0.10	0.55		INTEGRIN; CHAIN: A; COLLAGEN; CHAIN: B, C, D;	INTEGRIN INTEGRIN, COLLAGEN
1087	1d2i	A	361	534	1.4e-28	0.23	1.00		INTEGRIN; CHAIN: A; COLLAGEN; CHAIN: B, C, D;	INTEGRIN INTEGRIN, COLLAGEN
1087	1fhs	A	355	549	7e-51	0.29	0.49		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
1087	1ido		361	542	4.2e-35	0.13	0.48		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1087	1lfa	A	361	547	7e-32	-0.04	0.46		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1087	1qc5	A	361	543	5.6e-30	0.33	0.77		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B; CYCLODEXTRIN GLYCOSYLTRANSFERASE; ICIU 6 CHAIN: NULL; ICIU 7	CELL ADHESION INTEGRIN, CELL ADHESION
1088	1ciu		6	675	1.4e-77			82.96	GLYCOSIDASE CGTASE; ICIU 8 THERMOSTABLE ICIU 14	
1088	1e43	A	9	484	9.8e-17			79.59	ALPHA-AMYLASE; CHAIN: A;	HYDROLASE HYDROLASE, AMYLASE, FAMILY 13
1088	1gcy	A	1	397	5.6e-18			74.07	GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE; CHAIN: A;	HYDROLASE BETA-ALPHA-BARREL, BETA SHEET
1088	1hxo	A	5	488	5.6e-43			66.82	ALPHA AMYLASE (PPA); CHAIN: A;	HYDROLASE ALPHA-AMYLASE, INHIBITOR, CARBOHYDRATE, PANCREAS
1088	1qho	A	12	671	4.2e-70			81.19	ALPHA-AMYLASE; CHAIN: A;	HYDROLASE "MALTOGENIC" ALPHA AMYLASE; AMYLASE, GLYCOSIDE HYDROLASE, STARCH DEGRADATION
1088	1uok		110	675	0			90.36	OLIGO-1,6-GLUCOSIDASE; CHAIN: NULL;	GLUCOSIDASE GLUCOSIDASE, SUGAR DEGRADATION, HYDROLASE, TIM-BARREL 2
1088	1uok		7	543	0			74.70	OLIGO-1,6-GLUCOSIDASE; CHAIN: NULL;	GLUCOSIDASE GLUCOSIDASE, SUGAR DEGRADATION, HYDROLASE, TIM-BARREL 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1090	1aab		675	754	1.4e-17	0.90	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	GLYCOSIDASE, HYDROLASE
1090	1aab		676	754	1.7e-23	0.83	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMG A DNA-BINDING HMG-B BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMG-B BOX 1AAB 20
1090	1cgb	A	669	751	4.2e-25	0.51	1.00		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
1090	1cgt	A	680	748	1.4e-14	0.29	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(DDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1090	1cgt	A	681	748	3.4e-20	0.47	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(DDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMG-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1090	1hme		676	751	5.6e-29	0.50	1.00		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMG B) (DNA-BINDING 1HME 3 HMG-B BOX DOMAIN B OF RAT HMG1) (NMR, 1 STRUCTURE) 1HME 4	
1090	1hsm		679	752	2.8e-27	0.68	1.00		DNA-BINDING HIGH	

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH IISM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) IISM 4	
1090	1qrv	A	678	752	1.4e-17	0.65	1.00		DNA (5'- D(*G*CP*GP*AP*TP*AP *TP*CP*GP*C)-3'); CHAIN: C, D, HIGH MOBILITY GROUP PROTEIN D; CHAIN: A, B;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMG-D
1091	1d5s	B	342	382	5.6e-13			61.26	P1-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1091	1d5s	B	646	686	1.2e-14	-0.81	0.75		P1-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1091	1d5s	B	646	686	9.8e-13	-0.81	0.75		P1-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1091	1ezx	A	12	346	0			370.31	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1091	1ezx	A	316	650	0			366.89	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1091	1ezx	A	317	650	0	0.69	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1091	1ezx	B	651	686	1.1e-11	-0.78	0.30		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1091	1ezx	B	651	686	3.4e-12	-0.78	0.30		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1091	1qlp	A	11	382	0			424.42	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1- ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1091	1qlp	A	315	686	0			424.95	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1- ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1091	1qlp	A	317	686	0	0.82	1.00		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1- ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1091	1qmb	B	341	382	1.4e-12			61.02	ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-Pi; SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
1091	1qmb	B	645	686	2.8e-12	-0.81	0.90		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-Pi; SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
1091	1qmb	B	645	686	5.1e-14	-0.81	0.90		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-Pi; SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
1092	1a0j	A	330	536	1.4e-69	0.19	0.65		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1092	1a0l	A	330	530	1.4e-67	0.07	0.76		BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1092	1bru	P	330	536	2.8e-69	0.21	0.49		ELASTASE; CHAIN: P;	SERINE PROTEASE PPE, SERINE PROTEASE, HYDROLASE
1092	1ddj	A	328	536	7e-70	0.32	0.93		PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
1092	1dle	A	339	430	2.8e-17	0.39	-0.09		COMPLEMENT FACTOR B; CHAIN: A, B;	HYDROLASE SERINE PROTEASE, COMPLEMENT SYSTEM, FACTOR B, PROTEIN-2 PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										INTERACTION, ACTIVATION MECHANISM, BETA-BARREL FOLD,
1092	1dle	A	476	534	1.3e-07	-0.21	0.21		COMPLEMENT FACTOR B; CHAIN: A, B;	HYDROLASE SERINE PROTEASE, COMPLEMENT SYSTEM, FACTOR B, PROTEIN-2 PROTEIN INTERACTION, ACTIVATION MECHANISM, BETA-BARREL FOLD,
1092	1elv	A	352	497	0.0034	0.17	0.89		COMPLEMENT C1S COMPONENT1; CHAIN: A;	HYDROLASE TRYPsin-LIKE SERIN PROTEASE, CCP (OR SUSHI OR SCR)MODULE
1092	1f7z	A	330	536	1.4e-67	0.34	0.95		TRYPsin II, ANIONIC; CHAIN: A; PANCREATIC TRYPsin INHIBITOR; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR BPTI SERINE PROTEASE, TRYPsin PRECURSOR
1092	1fh8	A	331	497	0.0017	0.66	0.84		TRYPsin; CHAIN: A; GLY-ALA-ARG; CHAIN: B;	HYDROLASE BETA BARREL
1092	1fmi	A	330	536	1.3e-71	0.09	0.77		TRYPsin; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
1092	1qtf	A	357	532	3.4e-09	0.41	0.19		EXFOLIATIVE TOXIN B; CHAIN: A;	HYDROLASE, TOXIN EPIDERMOLYTIC TOXIN B; SERINE PROTEASE, SUPERANTIGEN, HYDROLASE, TOXIN
1092	1slw	B	330	536	5.6e-67	0.29	0.60		ECOTIN; CHAIN: A; ANIONIC TRYPsin; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPsin INHIBITOR, SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1092	1tm	A	330	536	1.4e-70	0.30	0.43		HYDROLASE (SERINE PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR ITRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) ITRN 4 HUMAN TRYPSIN, DFP INHIBITED ITRN 6	
1092	2sfa		357	532	1.7e-13	0.47	0.62		SERINE PROTEINASE; CHAIN: NULL;	HYDROLASE HYDROLASE, SERINE PROTEASE
1092	2sta	E	330	534	1.4e-68	0.17	0.76		TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: I	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
1092	5ptp		330	536	2.8e-65	0.09	0.51		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1103	1d2t	A	27	242	3.4e-39	0.45	0.78		ACID PHOSPHATASE; CHAIN: A;	HYDROLASE ALL ALPHA
1104	1cdq		36	112	2.8e-21			142.48	COMPLEMENT REGULATORY PROTEIN CD59 (NMR, 20 STRUCTURES) 1CDQ 3	
1104	1cdy		59	166	1e-08	0.23	-0.14		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1104	1erg		36	105	1.4e-20			132.21	COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1104	1P97	A	1	89	1.4e-33			54.30	CDS9 (EXTRACELLULAR 1ERG 3 REGION, RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1P97	A	65	274	8.4e-52			269.92	JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1P97	A	67	272	8.4e-52	0.92	1.00		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1P97	A	67	274	3.4e-51	0.90	1.00		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1104	1wio	A	75	312	6.8e-28	0.01	-0.18		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1105	1i5j	A	20	86	1.4e-29			87.22	APOLIPOPROTEIN CII; CHAIN: A;	LIPID TRANSPORT APOC-II; PROTEIN-LIPID INTERACTION, AMPHIPATHIC ALPHA HELIX
1105	1i5j	A	71	137	1.2e-30	-0.93	0.77		APOLIPOPROTEIN CII; CHAIN: A;	LIPID TRANSPORT APOC-II; PROTEIN-LIPID INTERACTION, AMPHIPATHIC ALPHA HELIX

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1105	1i5j	A	71	137	1.2e-30			86.49	APOLIPROTEIN CII, CHAIN: A;	LIPID TRANSPORT APOC-II; PROTEIN-LIPID INTERACTION, AMPHIPATHIC ALPHA HELIX
1105	1i5j	A	71	137	7e-29	-0.93	0.77		APOLIPROTEIN CII, CHAIN: A;	LIPID TRANSPORT APOC-II; PROTEIN-LIPID INTERACTION, AMPHIPATHIC ALPHA HELIX
1106	1h6q	A	1	159	2.8e-60	0.40	1.00		TRANSLATIONALLY CONTROLLED TUMOR PROTEIN; CHAIN: A;	TUMOR-ASSOCIATED PROTEIN TCTP, P23FYF; TUMOR-ASSOCIATED PROTEIN, FUNCTION UNKNOWN
1106	1h6q	A	1	160	1.7e-58	0.37	1.00		TRANSLATIONALLY CONTROLLED TUMOR PROTEIN; CHAIN: A;	TUMOR-ASSOCIATED PROTEIN TCTP, P23FYF; TUMOR-ASSOCIATED PROTEIN, FUNCTION UNKNOWN
1107	1awc	B	300	393	0.00051	-0.29	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1107	1b1x	B	337	411	0.00034	-0.03	0.09		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1107	1dcq	A	337	397	0.00051	0.15	0.64		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1107	1ikn	D	337	394	0.00085	-0.47	0.55		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D, TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1107	1myo		337	394	0.00068	0.18	0.11		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1107	1nfi	E	345	398	0.001	-0.25	0.84		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1107	1yes	B	337	423	0.00017	-0.05	0.03		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1108	1d2h	A	108	240	1.4e-18	-0.26	0.06		GLYCINE N-METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1109	1aj4		16	168	2.8e-26			99.38	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1109	1aj4		97	222	2.8e-26	0.11	0.46		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1109	1ak8		3	74	5.6e-32			59.57	CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC-DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
1109	1ap4		20	96	1.1e-18	0.79	1.00		CARDIAC N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTION
1109	1au1	B	18	179	2.8e-16			75.78	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1109	1avs	A	1	76	2.8e-28			54.68	TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
1109	1blq		1	78	8.4e-29			50.01	N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN SNTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
1109	1br1	B	26	166	1.3e-38	0.63	1.00		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1109	1br1	B	26	166	1.3e-38			92.46	MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1109	1br1	B	97	209	1.4e-11	0.24	0.22		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1109	1cdm	A	102	209	1.3e-29	-0.08	0.19		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM3	

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1109	1cdm	A	26	164	8.4e-59	0.72	1.00		CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
									CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3	
									CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1109	1cdm	A	26	164	8.4e-59			118.25	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3	
									CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4	
1109	1cll		102	209	9.8e-36	-0.05	0.24		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1109	1cll		15	91	1.4e-19	0.39	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1109	1cll		1	86	1.4e-42			50.32	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1109	1cll		26	164	5.6e-65	0.73	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1109	1cll		26	165	5.6e-65			135.44	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1109	1cmf		15	87	1.4e-05			70.55	CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1109	1dgu	A	12	177	8.4e-16			64.07	CALCIUM-SATURATED CIB; CHAIN: A	BLOOD CLOTTING HELICAL, EF-HANDS, BLOOD CLOTTING
1109	1dtl	A	20	165	2.8e-26			91.37	CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1109	1dtl	A	97	222	2.8e-26	0.36	0.63		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1109	1ext	A	102	209	2.8e-33	0.04	0.29		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ext	A	15	90	4.2e-18	0.29	0.95		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ext	A	24	163	1.4e-62	0.75	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ext	A	24	165	1.4e-62			132.92	CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1109	1ftq	A	3	130	3.4e-10	-0.15	0.30		GRANCALCIN; CHAIN: A, B;	METAL TRANSPORT PENTA-EF-HAND PROTEIN, CALCIUM BINDING PROTEIN
1109	1fpw	A	48	216	8.4e-19	-0.21	0.37		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	METAL BINDING PROTEIN YEAST FREQUENIN EF-HAND, CALCIUM
1109	1fw4	A	20	84	1.4e-05			67.19	CALMODULIN; CHAIN: A;	METAL BINDING PROTEIN EF-HAND, HELIX-LOOP-HELIX, FRAGMENT, CALCIUM, TR2C, C-2 TERMINAL DOMAIN, CALMODULIN
1109	1g8i	A	6	180	7e-14			65.19	NEURONAL CALCIUM SENSOR 1; CHAIN: A, B;	METAL BINDING PROTEIN FREQUENIN; CALCIUM BINDING-

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1109	1gzw	A	28	166	7e-11			89.53	CDCA4P; CHAIN: A;	PROTEIN, EF-HAND, CALCIUM ION
										CYTOKINE EF-HAND PROTEIN, MYOSIN LIGHT CHAIN; LIGHT CHAIN, CYTOKINESIS, CELL CYCLE, EF-HAND
1109	1hqy	A	15	203	2.8e-23			60.78	PROGRAMMED CELL DEATH PROTEIN 6; CHAIN: A;	APOPTOSIS PROBABLE CALCIUM-BINDING PROTEIN ALG-2; PENTA-EF-HAND PROTEIN, CALCIUM BINDING PROTEIN
1109	1hqy	A	37	194	2.8e-23	0.19	0.24		PROGRAMMED CELL DEATH PROTEIN 6; CHAIN: A;	APOPTOSIS PROBABLE CALCIUM-BINDING PROTEIN ALG-2; PENTA-EF-HAND PROTEIN, CALCIUM BINDING PROTEIN
1109	1iku		5	191	5.6e-11			58.57	RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1109	1tcf		102	224	7e-30	0.06	0.40		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE
										CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION
										REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1109	1tcf		17	165	7e-30			104.72	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE
										CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION
										REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1109	1top		102	224	2.8e-30	0.15	0.87		CONTRACTILE SYSTEM	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTEIN TROPONIN C 1TOP 3	
1109	1top		13	168	2.8e-30			107.77	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1109	1trc	A	19	86	1.4e-05			63.97	CALCIUM BINDING PROTEIN CALMODULIN (1R=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1109	1trf		5	76	2.8e-28			53.23	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	
1109	1vrk	A	102	209	2.8e-34	0.24	0.57		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1vrk	A	15	93	1.1e-18	0.39	0.99		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1vrk	A	23	166	9.8e-64	0.60	1.00		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1vrk	A	24	166	9.8e-64			133.11	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX,

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1109	1wdc	B	1	89	7e-20			67.20	SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1109	1wdc	B	26	168	1.7e-43			163.19	SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1109	1wdc	B	26	168	5.6e-35	0.48	1.00		SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1109	1wdc	B	28	166	1.7e-43	0.52	1.00		SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1109	1wdc	C	26	169	1.3e-06			89.97	SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1109	2mys	B	1	90	2.8e-18			51.56	MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mys	B	26	166	1.7e-38	-0.25	1.00		MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mys	B	26	169	1.7e-38			146.55	MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mys	B	7	78	5.6e-22			50.77	MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN

Table 5

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1109	2mys	B	96	198	5.6e-17	-0.25	0.05		MYOSIN; CHAIN: A, B, C ₃	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mys	C	29	165	2.8e-35			87.97	MYOSIN; CHAIN: A, B, C ₃	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1109	2mys	C	32	165	2.8e-35	-0.05	1.00		MYOSIN; CHAIN: A, B, C ₃	MUSCLE PROTEIN MUSCLE PROTEIN, MYOSIN SUBFRAGMENT-1, MYOSIN HEAD, 2 MOTOR PROTEIN
1112	1ajj		116	151	5.1e-09	-0.28	0.13		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: NULL;	RECEPTOR LR5; RECEPTOR, LDL RECEPTOR, CYSTEINE-RICH MODULE, CALCIUM
1112	1ajj		117	151	5.6e-09	-0.06	0.01		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: NULL;	RECEPTOR LR5; RECEPTOR, LDL RECEPTOR, CYSTEINE-RICH MODULE, CALCIUM
1112	1f8z	A	117	151	1.3e-07	-0.12	0.06		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR, LIGAND-BINDING DOMAIN, CALCIUM-BINDING, 2 FAMILIAL
1112	1ldl		116	151	5.1e-07	0.29	0.33		LOW-DENSITY LIPOPROTEIN RECEPTOR; LDL 4 CHAIN: NULL; LDL 5	BINDING PROTEIN LB1; LDL 7 LDL RECEPTOR CYSTEINE-RICH REPEAT LDL 15
1112	1sfp		1	113	8.4e-07	0.35	0.04		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1112	1sfp		26	114	1.7e-10	0.37	0.09		ASFP; CHAIN: NULL;	PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
										SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1112	1spp	A	26	112	8.5e-09	0.35	0.30		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)
1112	1spp	B	26	112	5.1e-10	0.17	0.11		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)
1119	1eis	A	277	354	9.8e-07	0.46	-0.09		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1119	9wga	A	485	655	4.2e-11	0.19	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1119	9wga	A	915	1107	1.4e-13	0.04	-0.19		LECTIN (AGGLUTININ) WHEAT GERM	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1123	1e08	A	1	325	0			152.98	AGGLUTININ (ISOLECTIN 2) 9WGA 3	
									[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]-HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
1123	1hfe	L	1	325	0			137.95	FE-ONLY HYDROGENASE (SMALLER SUBUNIT); CHAIN: S, T; FE-ONLY HYDROGENASE (LARGER SUBUNIT); CHAIN: L, M;	HYDROGENASE FE-ONLY HYDROGENASE, X-RAY CRYSTALLOGRAPHY, HYDROGENE 2 METABOLISM, PERIPLASM
1123	1jef	A	8	217	0.0068			51.59	SENSORY RHODOPSIN II; CHAIN: A;	SIGNALING PROTEIN SENSORY RHODOPSIN, MEMBRANE PROTEIN, PHOTOTAXIS RECEPTOR
1124	1dv8	A	199	326	5.6e-34	-0.18	0.33		ASIALOGLYCOPROTEIN RECEPTOR I; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN II; C-TYPE LECTIN CRD
1124	1hq8	A	194	308	5.6e-28			86.06	NKG2-D; CHAIN: A;	APOPTOSIS HOMODIMER, CIS-PROLINE
1124	1hvr	A	193	315	2.8e-26			100.53	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-RELATED PROTEIN A; CHAIN: C;	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE-LECTIN LIKE, MIC-2 A, MHC-1, COMPLEX, IMMUNE SYSTEM
1124	1hvr	A	48	163	1.4e-27			94.69	NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN; CHAIN: B, A; MHC CLASS I CHAIN-	IMMUNE SYSTEM NKG2D; MIC-A, MIC, PERB1; ACTIVATING NK CELL RECEPTOR, NKG2D, C-TYPE-LECTIN LIKE, MIC-2 A,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RELATED PROTEIN A; CHAIN: C;	MHC-I, COMPLEX, IMMUNE SYSTEM
1125	12e8	L	71	269	9.8e-17			73.24	2B8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1125	12e8	L	83	267	9.8e-17	0.28	0.75		2B8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1125	1adq	L	72	258	2.8e-22	0.38	1.00		IGG4 REA; CHAIN: A; RF- AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1125	1adq	L	72	271	2.8e-22			72.32	IGG4 REA; CHAIN: A; RF- AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1125	1b2w	L	70	269	4.2e-20			73.56	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X- RAY STRUCTURE, THREE- DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1125	1b6d	A	70	269	7e-21			73.38	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1125	1b1h	A	2	362	1.3e-43	0.06	0.99		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	1b1h	A	2	364	1.3e-43			121.44	HEMOLIN; CHAIN: A, B;	HOMOPHILIC ADHESION
1125	1b1h	A	73	386	5.1e-38	0.18	0.77		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1125	1b1l	J	76	267	1.4e-21	0.10	0.89		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1125	1b1l	H	84	268	9.8e-14	0.01	0.34		COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME 1BQL 3 1BQL 95	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1125	1b27	A	70	265	4.2e-19			73.01	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1125	1c1c	A	83	267	5.6e-17	0.35	0.82		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D; AXONIN-1; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE
1125	1cs6	A	10	363	5.6e-41	0.10	0.86			CELL ADHESION NEURAL CELL ADHESION

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	1cs6	A	15	364	1e-43			99.18	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1125	1cs6	A	66	429	5.6e-40	0.19	0.76		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1125	1cs6	A	72	379	1e-43	0.09	0.16		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1125	1cvs	C	169	362	4.2e-38	0.15	0.48		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1cvs	C	6	167	8.4e-20	0.01	-0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1cvs	C	81	270	4.2e-22	0.02	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1cvs	D	169	362	1.3e-39	0.32	0.80		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	1evs	D	6	167	2.8e-20	-0.26	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1125	1d5i	L	70	269	4.2e-21			72.82	CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
1125	1dfb	L	70	269	8.4e-22			75.44	IMMUNOGLOBULIN 3D6	
1125	1dfb	L	76	267	8.4e-22	0.36	0.99		IMMUNOGLOBULIN 3D6	
1125	1dgi	R	58	362	3.4e-51			111.26	POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1125	1dgi	R	75	362	3.4e-51	-0.21	0.46		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1125	1dgi	R	76	362	1.4e-39	-0.02	0.06		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	1epf	A	165	352	1.7e-28	0.36	0.55		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1125	1epf	A	175	346	2.8e-19	0.37	0.94		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1epf	A	3	152	2.8e-15	-0.07	0.00		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1epf	A	72	272	4.2e-24	-0.00	0.16		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1125	1ev2	B	170	362	2.8e-34	0.04	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD
1125	1ev2	G	170	366	4.2e-37	0.30	0.70		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD
1125	1evt	C	169	362	2.8e-39	0.03	0.51		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOIL FOLD
1125	1f2g	A	26	171	2.8e-12	-0.13	0.07		HIGH AFFINITY	IMMUNE SYSTEM FC-EPSILON R1-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1125	1f6a	A	166	365	3.4e-27	0.26	0.18		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1125	1f6a	A	171	346	1.4e-14	0.40	0.99		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1125	1f97	A	181	362	5.1e-26	0.27	0.11		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1125	1f97	A	5	158	2.8e-12	-0.05	0.09		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1125	1f97	A	77	265	4.2e-30	0.09	0.86		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1125	1f6g	A	170	362	8.5e-28	0.14	0.39		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1125	1f6g	A	272	362	1.5e-17	0.48	0.74		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	1fhg	A	275	362	2.8e-17	0.38	0.72		TELOKIN; CHAIN: A	BARREL CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1125	1fhg	A	78	167	5.6e-13	0.02	0.33		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1125	1fml	A	167	362	3.4e-26	0.21	0.01		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1125	1fml	A	273	375	1.7e-16	0.34	-0.06		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1125	1g0x	A	167	356	6.8e-24	0.23	0.05		LEUCOCYTE IMMUNOGLOBULIN- LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUCOCYTE INHIBITORY RECEPTOR-1; LEUCOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1125	1iai	L	83	267	9.8e-15	0.12	0.27		IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS IIAI 5 CHAIN: L, H; IIAI 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); IIAI 9 CHAIN: M, I IIAI 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1125	1ie5	A	269	362	8.4e-18	-0.11	0.45		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE IMMUNOGLOBULIN FOLD
1125	1ie5	A	272	363	6.8e-18	0.01	0.51		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE IMMUNOGLOBULIN FOLD
1125	1iil	G	164	366	6.8e-27	0.24	0.46		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF- 2, BASIC FIBROBLAST GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1125	1hi1	G	170	366	1.4e-36	0.38	0.53		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1125	1hi1	G	275	365	1.5e-16	0.61	0.55		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1125	1iib	B	79	366	3.4e-37			82.33	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1125	Imco	H	1	363	9.8e-19			78.42	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION IMCO 3	
1125	1iif	E	74	267	1.1e-21	0.32	0.96		NI5 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	1osp	L	70	269	1.1e-17			75.72	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN OSPA; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1, BORRELLIA BURGDORFERI 3 STRAIN B31
1125	1vca	A	73	278	8.5e-27	0.57	0.93		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1.2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1125	1wio	A	76	442	1.5e-35			89.83	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1125	2dli	A	167	354	8.5e-23	0.17	0.00		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1125	2fcb	A	170	365	1.5e-27	-0.16	0.75		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1125	2fcb	A	278	375	1.5e-16	0.17	0.03		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1125	2fgw	L	76	267	1.1e-21	0.30	0.99		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	

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Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1125	2ncm		282	363	1.5e-17	0.42	0.29		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL,	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1125	3fct	A	73	269	1.4e-20			77.03	METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
1125	8fab	A	73	268	5.6e-23			74.31	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
1125	8fab	A	75	258	5.6e-23	0.42	1.00		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HLL) 8FAB 3	
1126	1b3u	A	22	571	4.5e-18	0.11	-1202.08		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1126	1ec4	A	389	777	4.5e-21	0.35	-1202.08		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1126	1g3j	C	462	799	3e-15	0.02	-1202.08		BETA-CATENIN	TRANSCRIPTION BETA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ARMADILLO REPEAT REGION; CHAIN: A, C; TCF3-CBD (CATENIN BINDING DOMAIN); CHAIN: B, D;	CATENIN/TCF-3, PROTEIN-PROTEIN COMPLEX
1126	1i7w	A	462	915	1.5e-21	0.09	-1202.08		BETA-CATENIN; CHAIN: A, C; EPIHELIAL-CADHERIN; CHAIN: B, D;	CELL ADHESION E-CADHERIN; E-CADHERIN, CELL ADHESION, BETA-CATENIN, PROTEIN-PROTEIN 2 COMPLEX, EXTENDED INTERFACE, ARMADILLO REPEAT, PHOSPHOSERINE
1126	1ial	A	456	901	1.5e-18	0.14	-1202.08		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1126	3bet		412	787	6e-17	0.11	-1202.08		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1127	1a7q	L	27	132	0.00012			60.18	MONOCLONAL ANTIBODY D1.3; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, VARIANT
1127	1aif	A	27	211	0.0015			61.80	ANTI-IDIOTYPIC FAB 409.5.3 (GG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
1127	1bw ^w	A	25	133	0.00045			61.39	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENGE-JONES 2 PROTEIN, IMMUNE SYSTEM
1127	1cdy		35	136	1.5e-09	0.41	-1202.08		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									AXONIN-1; CHAIN: A;	TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1127	1es6	A	26	159	6e-08	0.25	-1202.08			CELL ADHESION NEURAL CELL ADHESION
1127	1evs	C	9	112	1.5e-11	0.04	-1202.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1127	1df9	A	37	134	4.5e-08	0.35	-1202.08		T LYMPHOCYTE ACTIVATION ANTIGEN; CHAIN: A;	IMMUNE SYSTEM B7-1 (CD80); IG SUPERFAMILY
1127	1eaj	A	28	132	7.5e-11	0.41	-1202.08		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
1127	1epf	A	31	112	6e-10	0.47	-1202.08		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1127	1f97	A	30	112	1.5e-10	0.12	-1202.08		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1127	1g9m	L	27	210	3e-06			61.27	ENVELOPE GLYCOPROTEIN GP120; CHAIN: G; T-CELL SURFACE	VIRUS/VIRAL PROTEIN COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GLYCOPROTEIN CD4; CHAIN: C; ANTIBODY 17B, LIGHT CHAIN; CHAIN: L; ANTIBODY 17B, HEAVY CHAIN; CHAIN: H;	FROM LABORATORY-ADAPTED ISOLATE, HXBC2, 3 SURFACE T-CELL GLYCOPROTEIN CD4, ANTIGEN-BINDING FRAGMENT 4 OF HUMAN IMMUNOGLOBULIN 17B
1127	1lxm	B	32	142	6e-10	0.32	-1202.08		GAMMA-DELTA T-CELL RECEPTOR; CHAIN: A, C, E, G; GAMMA-DELTA T-CELL RECEPTOR; CHAIN: B, D, F, H;	IMMUNE SYSTEM T-CELL RECEPTOR DELTA CHAIN; T-CELL RECEPTOR GAMMA CHAIN; IG DOMAIN, T CELL RECEPTOR, TCR, GDIOR
1127	1lgn	L	27	140	7.5e-05			60.22	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT IIGM 3	
1127	1neu		31	132	1.2e-09	0.36	-1202.08		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, STRUCTURAL PROTEIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD, SIGNAL, MYELIN 2 MEMBRANE ADHESION MOLECULE
1127	1nkr		29	148	1.5e-09	0.16	-1202.08		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR, INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1127	1vca	A	31	134	1.5e-10	0.22	-1202.08		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1131	1a25	A	648	768	1.4e-17	0.24	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1131	1a25	A	667	754	1.5e-18	0.08	-1202.08		PROTEIN KINASE C (BET A); CHAIN: A, B;	CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1131	1b9n	A	648	768	8.4e-23	0.21	-1202.08		SYNAPTOTAGMIN I; CHAIN: A;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1131	1c1y	A	666	786	1.4e-08	0.16	-1202.08		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1131	1dix	B	845	1047	2.8e-12	0.01	-1202.08		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1131	1d5y	A	647	781	5.6e-21	0.23	-1202.08		PROTEIN KINASE C, ALPHA TYPE, CHAIN: A;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1131	1rlw		664	754	4.5e-19	0.04	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL.SERINE, PROTEIN KINASE C
1131	1rlw		664	754	4.5e-19	0.04	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1131	1rlw		666	765	2.8e-08	0.14	-1202.08		PHOSPHOLIPASE A2;	HYDROLASE CALB DOMAIN;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1131	1rsy		619	754	3e-20	0.22	-1202.08		CHAIN: NULL; CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	HYDROLASE, C2 DOMAIN, CALB DOMAIN
1131	1rsy		648	768	8.4e-23	0.11	-1202.08		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1131	3tpb	A-	650	779	9.8e-17	0.29	-1202.08		RABPHILIN 3-A; CHAIN: A; RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1133	1f88	A	54	378	1e-24			73.00	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1133	1f88	B	54	371	3e-18			70.57	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1133	1hme		6	81	1.1e-28			98.43	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING 1HME 3 HMGB-BOX DOMAIN B OF RAT HMGI) (NMR, 1 STRUCTURE) 1HME 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1133	1hsm		9	87	1.1e-26			97.62	DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH 1HSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) 1HSM 4	
1134	1fx8	A	85	333	1.4e-47			73.96	GLYCEROL UPTAKE FACILITATOR PROTEIN; CHAIN: A;	MEMBRANE PROTEIN GLPF; GLYCEROL-CONDUCTING MEMBRANE CHANNEL PROTEIN
1138	1914		1	104	9.8e-36			69.38	SIGNAL RECOGNITION PARTICLE 9/14 FUSION PROTEIN; CHAIN: NULL;	ALU DOMAIN SRP9/14, ALU BM, RBD; ALU DOMAIN, CRYSTAL STRUCTURE; RNA BINDING, SIGNAL 2 RECOGNITION PARTICLE (SRP), TRANSLATION REGULATION
1138	1dhp	A	35	327	1.4e-91	0.66	-1202.08		DIHYDRODIPICOLINATE SYNTHASE; CHAIN: A;	SYNTHASE DHDP; SYNTHASE, DIHYDRODIPICOLINATE
1138	1dhp	A	35	327	1.4e-91			130.43	DIHYDRODIPICOLINATE SYNTHASE; CHAIN: A;	SYNTHASE DHDP; SYNTHASE, DIHYDRODIPICOLINATE
1138	1f6k	A	10	304	1.4e-69			123.19	N- ACETYLNEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE
1138	1f6k	A	33	327	3e-76			123.09	N- ACETYLNEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE
1138	1f6k	A	34	318	3e-76	0.52	-1202.08		N- ACETYLNEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE
1138	1f6k	A	34	323	5.6e-69	0.44	-1202.08		N- ACETYLNEURAMINATE LYASE; CHAIN: A, C;	LYASE BETA BARREL, LYASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ACETYLNEURAMINATE LYASE; CHAIN: A, C;	
1138	Inal	1	11	300	7e-64			121.57	N-ACETYLNEURAMINATE LYASE; INAL 4 CHAIN: 1, 2, 3, 4; INAL 5	LYASE
1138	Inal	1	34	318	4.5e-75	0.66	-1202.08		N-ACETYLNEURAMINATE LYASE; INAL 4 CHAIN: 1, 2, 3, 4; INAL 5	LYASE
1138	Inal	1	34	319	1.4e-63	0.61	-1202.08		N-ACETYLNEURAMINATE LYASE; INAL 4 CHAIN: 1, 2, 3, 4; INAL 5	LYASE
1138	Inal	1	34	323	4.5e-75			121.46	N-ACETYLNEURAMINATE LYASE; INAL 4 CHAIN: 1, 2, 3, 4; INAL 5	LYASE
1140	lhci	A	363	478	1.5e-08	0.04	-1202.08		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
1142	1dx5	1	176	284	1.4e-10	0.44	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C; D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; BGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1142	1dx5	I	252	353	5.6e-14	0.33	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR I-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1142	1dx5	I	320	427	5.6e-12	0.33	-1202.08		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR I-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1142	1hj7	A	214	288	1.4e-09	0.33	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1142	1hj7	A	368	427	1.3e-09	0.02	-1202.08		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1142	1llo		163	288	5.6e-09	0.18	-1202.08		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1142	1ptx	L	250	327	8.4e-09	0.09	-1202.08		FACTOR IXA; CHAIN: C, L; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1142	9wga	A	290	462	7e-15	0.01	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLLECTIN 2) 9WGA 3	CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1142	9wga	A	98	263	2.8e-15	-0.00	-1202.08		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLLECTIN 2) 9WGA 3	
1143	1f88	A	1	275	7e-82			58.80	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1143	1f88	A	25	366	1.4e-90			95.22	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1143	1f88	B	23	352	2.8e-82			66.80	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1145	1agc	A	661	780	6e-23	0.03	-1202.08		X11; CHAIN: A, B; PEPTIDE; CHAIN: C, D	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PEPTIDE BINDING 2 MODULE, PTB DOMAIN
1145	1ddm	A	484	618	1.5e-13	0.11	-1202.08		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1145	1ddm	A	661	778	4.5e-25	0.45	-1202.08		NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	SIGNALING DOMAIN (PTB), ASYMMETRIC CELL DIVISION
1145	1shc	A	477	620	9e-21	0.42	-1202.08		SHC; CHAIN: A; TRKA RECEPTOR PHOSHOPEPTIDE; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), PHOSPHOTYROSINE 2 BINDING DOMAIN (PTB)
1145	1x11	A	661	782	3e-23	0.20	-1202.08		X11; CHAIN: A, B; 13-MER PEPTIDE; CHAIN: C, D;	COMPLEX (PEPTIDE BINDING MODULE/PEPTIDE), PTB DOMAIN
1145	2nmb	A	661	786	7.5e-26	0.28	-1202.08		NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETRIC CELL DIVISION
1148	1a25	A	224	347	4.2e-24	0.06	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1148	1a25	A	72	191	4.2e-24	0.15	-1202.08		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1148	1bvn	A	69	185	8.4e-30	0.21	-1202.08		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTANSMTTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1148	1dix	A	255	356	2.8e-21	0.32	-1202.08		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1148	1dix	B	115	355	1e-31	0.00	-1202.08		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1148	1dix	B	255	356	2.8e-21	0.38	-1202.08		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1148	1dsy	A	70	194	4.2e-26	0.20	-1202.08		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYL-SERINE, PROTEIN KINASE C
1148	1tiw		240	331	1.5e-22	0.20	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1148	1rlw		90	181	8.4e-16	0.21	-1202.08		PHOSPHOLIPASE A2; CHAIN: NULL;	DOMAIN HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1148	3rpb	A	227	340	6e-24	0.05	-1202.08		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1148	3rpb	A	72	191	4.2e-20	0.10	-1202.08		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1149	1cex		8	53	0.0006	1.11	-1202.08		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1149	1kap	P	8	53	0.0015	1.00	-1202.08		ALKALINE PROTEASE; IKAP 4 CHAIN: P; IKAP 5 TETRAPEPTIDE (GLY SER ASN SER); IKAP 9 CHAIN: I; IKAP 10	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE PROTEASE; IKAP 6 CALCIUM BINDING PROTEIN IKAP 19
1149	1qg4	A	24	53	0.003	2.03	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1149	1tal		3	53	3e-05	1.40	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1149	1tal		3	70	0.003	0.91	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1149	1tal		8	63	0.00045	1.19	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1150	1cex		8	67	9e-06	1.25	-1202.08		CUTINASE; CHAIN: NULL;	PROTEINASE SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1150	1ga6	A	8	67	0.0006	0.92	-1202.08		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPERLIN, PEPSTATIN-INSENSITIVE SERINE- CARBOXYL PROTEINASE
1150	1qq4	A	24	53	0.003	2.03	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1150	1tal		24	67	3e-05	1.57	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1150	1tal		3	63	3e-07	1.27	-1202.08		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1152	1f88	A	107	436	1.5e-15			61.82	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1152	1f88	B	107	434	4.5e-13			68.15	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1153	1etj	A	24	362	5.6e-52	0.54	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1153	1etj	A	480	761	1.4e-55	0.10	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1;	TRANSCRIPTION INHIBITOR BETA-PROPELLER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1153	1ej	A	725	931	2.8e-21	0.11	-1202.08		CHAIN: A, B, C; TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1153	1ej	A	72	431	4.2e-50	0.16	-1202.08		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1153	1got	B	17	363	1.4e-58	0.36	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1153	1got	B	513	802	1.1e-43	0.10	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1153	1got	B	552	887	4.2e-34	0.10	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1153	1got	B	644	936	2.8e-28	0.31	-1202.08		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RETROPEPSIN; CHAIN: A, B;	SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1158	1b6l	A	176	280	4.2e-57	0.22	-1202.08		RETROPEPSIN; CHAIN: A, B;	HYDROLASE/HYDROLASE INHIBITOR HIV-1 PR; COMPLEX (ACID PROTEINASE/PEPTIDE)
1158	1bai	A	162	279	2.8e-17			55.92	ROUS SARCOMA VIRUS PROTEASE; CHAIN: A, B; INHIBITOR; CHAIN: C;	COMPLEX (PROTEASE/INHIBITOR) HUMAN IMMUNODEFICIENCY VIRUS PROTEASE, ROUS SARCOMA VIRUS 2 PROTEASE, CRYSTAL STRUCTURES, PROTEIN-MEDIATED INTERACTION, 3 VIRAL MATURATION, COMPLEX (PROTEASE/INHIBITOR) HEADER
1158	1bai	A	1	111	1.4e-24			52.01	ROUS SARCOMA VIRUS PROTEASE; CHAIN: A, B; INHIBITOR; CHAIN: C;	COMPLEX (PROTEASE/INHIBITOR) HUMAN IMMUNODEFICIENCY VIRUS PROTEASE, ROUS SARCOMA VIRUS 2 PROTEASE, CRYSTAL STRUCTURES, PROTEIN-MEDIATED INTERACTION, 3 VIRAL MATURATION, COMPLEX (PROTEASE/INHIBITOR) HEADER
1158	1bwb	A	176	280	1.4e-60	0.15	-1202.08		HIV-1 PROTEASE; CHAIN: A, B;	HYDROLASE HIV-1 PROTEASE, HYDROLASE
1158	1c6x	A	176	280	2.8e-60	0.42	-1202.08		PROTEASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1158	1daz	C	176	280	5.6e-58	0.29	-1202.08		PEPTIDE INHIBITOR; CHAIN: A, B; HIV-1 PROTEASE (RETROPEPSIN); CHAIN: C, D;	HYDROLASE HIV-1 PROTEASE, MUTANT, DIMER, INHIBITOR, OCCUPANCY
1158	1dun		44	161	7.5e-23			57.26	DEOXYURIDINE 5'-	HYDROLASE DUTPASE, DUTP

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									TRIPHOSPHATE NUCLEOTIDOHYDROLA SE; CHAIN: NULL;	PYROPHOSPHATASE; HYDROLASE, DUTPASE, ELAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1158	1dun		58	150	7.5e-23	0.91	-1202.08		DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLA SE; CHAIN: NULL;	HYDROLASE DUTPASE, DUTP PYROPHOSPHATASE; HYDROLASE, DUTPASE, ELAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1158	1dun		9	126	1.4e-18			56.78	DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLA SE; CHAIN: NULL;	HYDROLASE DUTPASE, DUTP PYROPHOSPHATASE; HYDROLASE, DUTPASE, ELAV, TRIMERIC ENZYME, ASPARTYL PROTEASE
1158	1euw	A	1	125	7e-22			61.05	DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLA SE; CHAIN: A;	HYDROLASE DUTPASE; JELLY ROLL, MERCURY DERIVATIVE
1158	1euw	A	32	160	4.5e-18			62.42	DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLA SE; CHAIN: A;	HYDROLASE DUTPASE; JELLY ROLL, MERCURY DERIVATIVE
1158	1euw	A	58	150	4.5e-18	0.76	-1202.08		DEOXYURIDINE 5'- TRIPHOSPHATE NUCLEOTIDOHYDROLA SE; CHAIN: A;	HYDROLASE DUTPASE; JELLY ROLL, MERCURY DERIVATIVE
1158	1f7d	A	43	157	1.2e-22			62.82	POL POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1158	1f7d	A	58	150	1.2e-22	0.83	-1202.08		POL POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1158	1f7d	A	8	122	1.4e-21			62.45	POL POLYPROTEIN; CHAIN: A, B;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA-BARREL
1158	1f7r	A	43	180	1.5e-24			73.37	POL POLYPROTEIN; CHAIN: A;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA BARREL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1158	1f7r	A	58	166	1.5e-24	0.29	-1202.08		POL POLYPROTEIN; CHAIN: A;	PROTEIN VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA BARREL PROTEIN
1158	1f7r	A	8	136	2.8e-26			71.47	POL POLYPROTEIN; CHAIN: A;	VIRUS/VIRAL PROTEIN EIGHT STRANDED BETA BARREL PROTEIN
1158	1fmb		176	280	2.8e-13			51.30	ELAV PROTEASE; CHAIN: NULL;	HYDROLASE (ACID PROTEINASE) HYDROLASE (ACID PROTEINASE), RNA-DIRECTED DNA POLYMERASE, 2 ASPARTYL PROTEASE, ENDONUCLEASE, POLYPROTEIN
1158	1g6l	A	170	280	2.8e-63	-0.00	-1202.08		HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1158	1g6l	A	93	280	2.8e-63			53.13	HIV-1 PROTEASE; CHAIN: A;	HYDROLASE HYDROLASE
1158	1hvc		148	280	1.4e-63	0.13	-1202.08		HYDROLASE(ACID PROTEASE) HIV-1 PROTEASE (TETHERED DIMER LINKED BY IHVC3 GLY-GLY-SER-SER-GLY) COMPLEXED WITH A-76928 IHVC 4	
1158	1hvc		60	280	1.4e-63			54.32	HYDROLASE(ACID PROTEASE) HIV-1 PROTEASE (TETHERED DIMER LINKED BY IHVC3 GLY-GLY-SER-SER-GLY) COMPLEXED WITH A-76928 IHVC 4	
1158	1ida	A	176	279	2.8e-37	0.08	-1202.08		HYDROLASE(ACID PROTEINASE) HUMAN IMMUNODEFICIENCY	

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1158	1s1p		176	280	1.4e-39	0.29	-1202.08		VIRUS TYPE 2 (HIV-2) PROTEASE 1IDA 3 COMPLEXED WITH THE INHIBITOR BILA 1906 CONTAINING THE 1IDA 4 HYDROXYETHYLAMINE DIPEPTIDE ISOSTERE 1IDA 5	
									HYDROLASE/ACID PROTEINASE) SIMIAN IMMUNODEFICIENCY VIRUS (SIV) PROTEINASE 1SIP 3 (SIV MAC251-32H ISOLATE) (E.C.3.4.23.-) 1SIP 4	
1167	1a8q		18	281	8.5e-47	-0.33	0.06		BROMOPEROXIDASE A1; CHAIN: NULL;	HALOPEROXIDASE CHLOROPEROXIDASE A1, HALOPEROXIDASE A1; HALOPEROXIDASE, OXIDOREDUCTASE
1167	1a8s		16	280	1.4e-46	-0.21	0.11		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE, OXIDOREDUCTASE, PROPIONATE COMPLEX
1167	1c4x	A	13	270	3.4e-37	-0.33	0.03		2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD, HYDROLASE, PCB DEGRADATION
1167	1c4x	A	6	282	3.4e-37			51.46	2-HYDROXY-6-OXO-6-PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD, HYDROLASE, PCB DEGRADATION
1167	1cqw	A	13	281	1.2e-35	-0.34	0.01		HALOALKANE DEHALOGENASE; 1-CHLOROHEXANE	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1214	1ev2	E	26	110	3.40E-17	-0.29	0.09		CHAIN: A; FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2, IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
1214	1ev2	G	26	110	3.40E-17	-0.61	0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2, FGFR2, IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREEFOLD FOLD
1214	1f2q	A	18	107	3.40E-18	0.04	0.93		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON R1-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1214	1f6a	A	18	106	5.10E-17	0.31	0.9		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IGE EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FCEPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1214	1fcg	A	9	103	1.00E-17	-0.14	0.23		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32, FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1214	1fhl	A	6	103	3.40E-16	-0.17	0.93		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1214	2fcb	A	9	105	8.50E-19	-0.14	0.17		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1247	1ec4	A	130	442	1.4e-09	-0.03	0.88		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	SYSTEM
1247	1ec4	A	168	498	9.8e-12	0.33	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1247	1lal	A	185	485	2.8e-11	0.11	0.95		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1247	2bct		390	501	0.00011	0.23	0.25		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-CATENIN, STRUCTURAL PROTEIN
1247	3bct		224	505	8.4e-11	0.28	0.99		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1273	1rfs		2	278	1.7e-62			329.79	SULFUR-SUBSTITUTED RHODANESE; CHAIN: NULL;	TRANSEFERASE TRANSFERASE, RHODANESE, SULFURTRANSFERASE
1294	1dx5	I	104	218	5.10E-10	0.02	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT
									THROMBIN INHIBITOR	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1294	1skz		49	163	5.10E-08	0.01	-0.11		L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H; ANTISTASIN; CHAIN: NULL;	COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1294	4mt2		71	127	1.70E-09	0.25	-0.12		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	SERINE PROTEASE INHIBITOR; FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1301	1bx2	A	133	183	2.9E-07	-0.58	0.39		HLA-DR2; CHAIN: A, D; HLA-DR2; CHAIN: B, E; HLA-DR2; CHAIN: C, F;	IMMUNE SYSTEM HLA-DR2, MYELIN BASIC PROTEIN, MULTIPLE SCLEROSIS, 2 AUTOIMMUNITY, IMMUNE SYSTEM
1301	1cql	A	132	182	4.3E-07	-0.56	0.05		CH3 DOMAIN OF MAK33 ANTIBODY; CHAIN: A, B;	IMMUNE SYSTEM CONSTANT DOMAIN, C1-SUBSET, IMMUNOGLOBULIN, IMMUNE SYSTEM
1301	1cvs	C	79	133	0.00048	-0.01	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1301	1dgi	R	20	190	9.6E-16	-0.60	0.00		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1301	1duz	A	126	183	4.8e-07	-0.51	0.84		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1301	1e4k	A	135	182	9.6e-08	-0.62	0.17		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
1301	1f5w	A	32	131	9.6e-09	0.47	0.94		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
1301	1f5w	A	92	132	0.00032	-0.20	0.37		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR IMMUNOGLOBULIN V DOMAIN FOLD, SYMMETRIC DIMER
1301	1fc2	D	135	182	1.4e-07	-0.48	0.40		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
1301	1iak	A	126	183	9.6e-08	-0.85	0.01		MHC CLASS II I-AK; CHAIN: A, B, P; HEN EGGWHITE LYSOZYME PEPTIDE	HISTOCOMPATIBILITY ANTIGEN I-AK HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
1301	1neu		34	133	4.8e-06	0.38	0.03		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, STRUCTURAL PROTEIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1333	1alh	A	142	221	3.4e-27	-0.80	0.12		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	SIGNAL, MYELIN 2 MEMBRANE ADHESION MOLECULE
1333	1alh	A	169	249	1.2e-29	0.01	0.88		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1333	1b6g		385	480	0.0016	0.76	0.74		HALOALKANE DEHALOGENASE; CHAIN: NULL;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1333	1mey	C	141	221	1.7e-45	-0.46	0.03		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	168	249	1.5e-48	-0.17	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	196	277	5.1e-50	0.21	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	1mey	C	224	305	8.5e-51	0.19	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FINGER PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	Imey	C	252	333	3.4e-51	0.40	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	Imey	C	252	334	3.4e-51			107.37	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	Imey	C	308	389	5.1e-51	0.30	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
									DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1333	Imey	C	336	415	8.5e-36	0.10	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
									PROLYL OLIGOPEPTIDASE; CHAIN: A;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA-2 PROPELLER
1333	1qfm	A	383	576	0.0002	0.23	0.28		THIA; CHAIN: A, D, 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION,
1333	1tff	A	169	314	8.5e-38	-0.13	0.86			

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1333	1tf6	A	171	333	4e-69	0.03	0.92		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	196	366	6e-79			110.10	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	197	342	5.1e-38	0.25	0.94		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	197	361	1.6e-78	-0.03	0.98		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	225	371	6.8e-39	0.23	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1333	1tf6	A	225	389	6e-79	0.09	0.89		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	253	389	1.7e-36	0.22	1.00		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	281	395	8e-49	0.28	0.86		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1tf6	A	281	471	1.4e-32	-0.28	0.09		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1333	1ubd	C	143	249	3.4e-33	-0.58	0.54		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1333	1ubd	C	171	277	8e-50	-0.10	0.98		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	(TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	176	277	5.1e-35	-0.02	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	194	306	2e-60			90.99	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	222	333	2e-60	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	232	333	3.4e-35	0.03	0.98		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	278	389	8e-60	0.18	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	1ubd	C	288	389	5.1e-35	0.28	1.00		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1333	2gli	A	110	248	1.7e-34	-0.15	0.27		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gli	A	169	307	6e-64	0.12	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gli	A	176	304	1e-34	0.20	1.00		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1333	2gli	A	196	335	4e-77			98.74	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gli	A	196	363	4e-77	0.14	0.81		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gli	A	252	390	1e-76	0.36	0.94		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1333	2gli	A	260	388	3.4e-34	0.08	0.94		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1334	1a0f	A	154	371	1.7e-24			55.32	GLUTATHIONE S-TRANSFERASE; CHAIN: A, B;	TRANSFERASE GST, GLUTATHIONE TRANSFERASE; TRANSFERASE, GLUTATHIONE CONUGATION, DETOXIFICATION,
1334	1aw9		160	374	1.2e-42	0.03	0.72		GLUTATHIONE S-TRANSFERASE III; CHAIN: NULL;	TRANSFERASE TRANSFERASE, HERBICIDE DETOXIFICATION
1334	1axd	A	160	366	5.1e-36	0.05	0.21		GLUTATHIONE S-TRANSFERASE I; CHAIN: A, B; LACTOYL-GLUTATHION B; CHAIN: C, D	COMPLEX (TRANSFERASE/LIGAND) COMPLEX (TRANSFERASE/LIGAND), TRANSFERASE, HERBICIDE 2 DETOXIFICATION HEADER
1334	1een	A	151	378	1e-36	0.22	0.23		GLUTATHIONE-S-TRANSFERASE; CHAIN: A;	TRANSFERASE GST, GLUTATHIONE CONUGATING, PUTATIVE OXIDOREDUCTASE
1334	1f3a	A	159	385	3.4e-38	0.09	0.75		GLUTATHIONE S-	TRANSFERASE GLUTATHIONE S-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									TRANSFERASE YA CHAIN: A, B;	TRANSFERASE, GLUTATHIONE
1334	1gsd	A	160	375	3.4e-35	0.09	0.86		GLUTATHIONE TRANSFERASE A1-1; 1GSD 5 CHAIN: A, B; 1GSD 6	TRANSFERASE (GLUTATHIONE)
1334	1gse	A	160	385	1.7e-36	0.11	0.75		GLUTATHIONE TRANSFERASE: 1GSE 6 CHAIN: A, B; 1GSE 7	TRANSFERASE (GLUTATHIONE) A1-1 1GSE 19
1334	1hna		160	380	3.4e-37	0.20	0.80		TRANSFERASE(GLUTATHIONE) GLUTATHIONE S-TRANSFERASE (HUMAN, CLASS MU) (GSTM2-2) 1HNA 3 FORM A (E.C.2.5.1.18) MUTANT WITH TRP 214 REPLACED BY PHE 1HNA 4 (W214F) 1HNA 5	
1334	6gsv	A	160	381	1.7e-37	0.04	0.33		MU CLASS GLUTATHIONE S-TRANSFERASE OF ISOENZYME CHAIN: A, B;	GLUTATHIONE TRANSFERASE RAT GST; GLUTATHIONE TRANSFERASE, ISOENZYME 3-3, T13S MUTANT
1348	1ad0	B	19	231	3.40E-70			88.97	FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
1348	1afv	H	258	443	1.70E-50	0.13	0		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1348	1aif	H	15	230	5.10E-71	0.1	0.01		ANT1-ID10TYPIC FAB	IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									409.5.3 (GGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN, C REGION, V REGION
1348	1ba1	L	146	328	6.80E-16	-0.04	0.17		IMMUNOGLOBULIN FAB FRAGMENT OF MURINE MONOCLONAL ANTIBODY AN02 COMPLEX 1BAF 3 WITH ITS HAPTEN (2,2,6,6-TETRAMETHYL-1-PIPERIDINYLOXY-1BAF 4 DINITROPHENYL) 1BAF 5	
1348	1bfo	B	19	230	1.50E-67			80.18	CAMPATH-1G ANTIBODY; CHAIN: A, B, C, D, E, F, G, H;	ANTIBODY ANTIBODY, FAB, CAMPATH-1G, CD52
1348	1bln	A	143	528	6.80E-26	0.01	0.7		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1348	1blh	A	44	443	1.40E-46			118.73	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1348	1blh	A	61	443	1.40E-46	0.23	0.57		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1348	1bln	B	15	232	1.70E-72	0.06	0.25		MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
1348	1bln	B	19	231	1.70E-72			79.05	MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN:	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1348	1cl7	I	158	235	3.40E-19	0.35	0.64		A, C, MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM
1348	1cl0	H	15	234	1.70E-72	-0.01	0.22		ASB7 MONOCLONAL ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN
1348	1cl0	H	19	233	1.70E-72			89.82	ASB7 MONOCLONAL ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FRAGMENT
1348	1clz	H	19	233	3.40E-69			83.21	IGG FAB (IGG3, KAPPA); CHAIN: L, H;	IMMUNOGLOBULIN MER96 FAB (IMMUNOGLOBULIN);
1348	1cs6	A	140	540	8.50E-38	0.02	0.49		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1348	1cs6	A	255	576	1.00E-30	-0.01	0.48		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1348	1cs6	A	40	444	5.10E-63	0.36	0.86		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1348	1cvs	C	137	341	3.40E-20	0.03	-0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										FACTOR/GROWTH FACTOR RECEPTOR
1348	1cvs	D	137	341	1.40E-21	0.19	0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1348	1d5i	H	258	454	6.80E-47	0.09	0.21		CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: I; CHIMERIC GERM LINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
1348	1dee	A	143	327	5.10E-18	-0.09	0.01		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
1348	1dftb	H	258	454	1.70E-47	-0.08	0.83		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
1348	1dftb	L	143	327	1.00E-19	-0.04	0.16		IMMUNOGLOBULIN 3D6 FAB 1DFB 3	
1348	1dgi	R	23	340	8.20E-38	0.13	0.01		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: I; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1348	1dn2	A	247	437	1.20E-39	0.07	-0.18		IMMUNOGLOBULIN LAMBDA HEAVY	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1348	1dzb	A	15	215	8.50E-58	0.23	-0.13		CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	
									SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYL MURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
1348	1dzb	A	256	425	3.40E-35	0.09	0.22		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYL MURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
1348	1evt	C	137	341	1.70E-21	0.22	0.04		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1348	1fs8	H	258	444	1.70E-49	-0.17	0.11		IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1348	1fai	H	258	440	1.50E-50	0.19	0.34		IMMUNOGLOBULIN FAB FRAGMENT FROM A MONOCLONAL ANTI-ARSONATE ANTIBODY,	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									R19.9 1FAI 3 (IGG2B,KAPPA) 1FAI 4 COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY F9.13.7 (GGI1) 1FBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) 1FBI 4	
1348	1fbi	H	258	440	1.70E-51	-0.06	0.12			
1348	1fcg	A	237	443	4.10E-20	0.26	0.51		FC RECEPTOR FC(GAMMA)RLA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1348	1fvg	H	19	233	5.10E-67			79.18	IMMUNOGLOBULIN/VIR US HEMAGGLUTININ IGG2A FAB FRAGMENT (FAB 26/9) COMPLEXED WITH INFLUENZA 1FRG 3 HEMAGGLUTININ HAI (STRAIN X47) (RESIDUES 101 - 108) 1FRG 4	
1348	1fvd	A	143	327	1.40E-17	-0.13	0.24		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1348	1fvd	B	258	454	6.80E-48	0.02	0.59		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1348	1hil	B	19	233	6.80E-71			79.17	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (FAB 17/9) 1HIL 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1348	1iai	H	13	231	1.70E-68			80.32	IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 11AI 5 CHAIN: L, H; 11AI 7 ANTI-IDIOTYPIC FAB 409.5.3 (GG2A); 11AI 9 CHAIN: M, I 11AI 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1348	1igc	H	16	235	1.40E-72	-0.02	0.07		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1348	1igc	H	258	444	3.40E-51	0.11	0.03		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1348	1igt	B	15	439	0	-0.02	0.13		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1348	1igt	B	23	441	0			124.15	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1348	1igy	B	14	441	0			114.03	IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1348	1ikt	H	256	444	3.40E-51	0.04	-0.08		COMPLEX (ANTIBODY/IMMUNOSUP	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(PRESSANT) IMMUNOGLOBULIN IGG1-KAPPA ANTIBODY FRAGMENT FAB COMPLEXED I1KF 3 WITH CYCLOSPORIN I1KF 4	
1348	1t1b	B	143	443	2.90E-21	0.12	0.47		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1348	1kel	H	19	230	1.20E-67			78.42	28B4 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, 2 IMMUNOGLOBULIN, CATALYTIC ANTIBODY
1348	1hl	A	148	336	1.00E-21	-0.08	0.19		LAMBDA III BENCE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENCE JONES PROTEIN
1348	1lmk	A	16	215	1.50E-52	0.06	-0.13		IMMUNOGLOBULIN ANTI- PHOSPHATIDYLINOSITO L SPECIFIC PHOSPHOLIPASE C DIABODY ILMK 3 SYNONYMS: L5MK16 DIABODY, SINGLE- CHAIN FV DIMER ILMK 4	
1348	1lmk	A	258	428	5.10E-33	0.1	0.34		IMMUNOGLOBULIN ANTI- PHOSPHATIDYLINOSITO	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									L.SPECIFIC PHOSPHOLIPASE C DIABODY 1LMK 3 SYNONYMS: L5MK16 DIABODY, SINGLE-CHAIN FV DIMER 1LMK 4	
1348	1mco	H	147	527	5.10E-35	-0.24	0.09		IMMUNOGLOBULIN (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1348	1mco	H	18	437	8.50E-98	0.03	0.27		IMMUNOGLOBULIN (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1348	1mco	H	20	442	8.50E-98			101.92	IMMUNOGLOBULIN (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1348	1mcp	H	256	429	5.10E-35	0.29	0.51		IMMUNOGLOBULIN FV FRAGMENT (MURINE SE155-4) COMPLEX WITH THE TRISACCHARIDE: IMFA 3 ALPHA-D-GALACTOSE(1-2)/ALPHA-D-ABEQUOSE(1-3)/ALPHA-	
1348	1mfa		148	352	6.80E-24	0.24	0.09		IMMUNOGLOBULIN FV FRAGMENT (MURINE SE155-4) COMPLEX WITH THE TRISACCHARIDE: IMFA 3 ALPHA-D-GALACTOSE(1-2)/ALPHA-D-ABEQUOSE(1-3)/ALPHA-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IMFA 4 D-MANNOSE (P1-OME) (PART OF THE CELL-SURFACE CARBOHYDRATE IMFA 5 OF PATHOGENIC SALMONELLA) IMFA 6	
1348	Inca	H	15	233	5.10E-67			78.54	HYDROLASE(O-GLYCOSYL) N9 NEURAMINIDASE-NC41 (E.C.3.2.1.18) COMPLEX WITH FAB INCA 3	
1348	Infcl	F	19	233	1.70E-70			83.51	N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; HS7 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGL OBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGL OBULIN)
1348	Ingp	H	15	233	1.70E-73	0.1	0.12		N1G9 (GGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,
1348	Inqb	A	258	425	1.70E-33	0.02	0.69		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
1348	Ipsk	H	258	438	6.80E-41	0.05	0.12		ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN FAB, GD2-GANGLIOSIDE, CARBOHYDRATE, MELANOMA, IMMUNOGLOBULIN
1348	Iqkz	H	16	233	6.80E-72	-0.09	0.12		ANTIBODY; CHAIN: H, L; PROTEIN G-PRIME; CHAIN: A; MAJOR OUTER MEMBRANE PROTEIN P1.16; CHAIN: P;	IMMUNE SYSTEM FAB, PORIN, NEISSERIA MENINGITIDIS, PORIN
1348	Iqok	A	15	220	3.40E-56	0.04	-0.13		MFE-23 RECOMBINANT	IMMUNOGLOBULIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
1348	1qok	A	256	430	1.70E-34	0.36	0.41		MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
1348	1r24	B	258	434	5.10E-45	0.24	0.3		IGG3-KAPPA ANTIBODY (LIGHT CHAIN); CHAIN: A, C; IGG3-KAPPA ANTIBODY (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM PRELIMINARY, IMMUNE SYSTEM
1348	1sbs	H	15	232	6.80E-72	0.23	0.54		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1348	1sbs	H	23	230	6.80E-72			80.32	MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1348	1sbs	H	258	440	1.20E-50	-0.02	0.1		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1348	1sm3	H	15	233	8.50E-73	-0.11	0		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPTOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPTOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
1348	1sm3	H	23	233	8.50E-73			79.3	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPTOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPTOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
1348	1tet	H	20	233	1.00E-65			78.05	IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33)	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									COMPLEX WITH CHOLERA 1TET 3 TOXIN PEPTIDE 3 (CTP3) 1TET 4 VH-P8; CHAIN: NULL;	
1348	1vhp		15	141	1.20E-47	0.11	-0.19			IMMUNOGLOBULIN NM8, VH DOMAIN, ANTIBODY, HUMAN, IMMUNOGLOBULIN
1348	1wio	A	98	428	8.20E-14	0.02	0.13		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1348	25c8	L	146	328	1.00E-15	0.01	-0.01		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1348	2ft4	H	258	453	6.80E-47	-0.01	0.33		IMMUNOGLOBULIN IMMUNOGLOBULIN FAB 2FB4 4	
1348	2ftj	H	256	429	1.70E-34	0.19	0.62		IMMUNOGLOBULIN IG* A FAB FRAGMENT (J539) (GALACTAN-BINDING) 2FBJ 3	
1348	2gtb	B	16	233	1.20E-73	0.09	0.53		IMMUNOGLOBULIN IGG2A FAB FRAGMENT (CNJ206) 2GFB 3	
1348	2hlp	H	256	440	6.80E-53	-0.14	0.07		2H1; CHAIN: L, H; PA1; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE) ANTIBODY STRUCTURE, CRYPTOCOCUS, PEPTIDE, PHAGE LIBRARY, 2 POLYSACCHARIDE, COMPLEX (ANTIBODY/PEPTIDE)
1348	6fab	H	258	444	6.80E-50	-0.07	0.06		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT OF THE MURINE ANTI-	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
									PHENYLARSONATE 6FAB 3 ANTIBODY 36-71, FAB 36-71 6FAB 4	
1348	8fab	A	148	336	3.40E-21	0.17	0.29		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN	
									IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1356	12e8	L	22	222	1.7e-17			74.09	2E8 (IGG1=KAPPA=) ANTIBODY; CHAIN: L, H, M, P;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1356	1a4j	L	22	222	1.5e-19			73.51	IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERM LINE
1356	1ad0	A	29	222	3.4e-22	0.15	0.35		FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
1356	1adq	L	25	224	1.4e-26			71.74	IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN), RHEUMATOID FACTOR 2
1356	1adq	L	28	219	1.4e-26	0.09	0.78		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIG EN), RHEUMATOID FACTOR 2
									AUTO-ANTIBODY COMPLEX	
1356	1b2w	L	22	222	1.4e-22			74.84	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
									CHAIN; CHAIN: H;	ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1356	1b2w	L	29	222	1.4e-22	0.10	0.80		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1356	1b4j	L	29	222	1.2e-21	-0.07	0.31		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
1356	1b6d	A	22	222	1.7e-22			74.61	IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1356	1b6d	A	29	222	1.7e-22	-0.03	0.69		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1356	1b6j	L	22	222	1e-19			80.38	IMMUNOGLOBULIN FAB FRAGMENT OF MONOCLONAL ANTIBODY B72.3 (BBJ 3 (MURINE/HUMAN CHIMERA) BBJ 4	
1356	1b1h	A	21	394	1.5e-55			115.28	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1356	1bhh	A	28	395	1.5e-55	0.01	0.07		HEMOLIN; CHAIN: A, B;	HOMOPHILIC ADHESION
1356	1bjl	L	22	222	1.4e-22			72.47	FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1356	1bjl	L	29	222	1.4e-22	0.02	0.39		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1356	1bpg	A	22	222	3.4e-19			73.26	ANTIBODY (CB 4-1); CHAIN: A, B; PEPTIDE; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSS REACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1, COMPLEX (ANTIBODY/PEPTIDE)
1356	1bz7	A	22	218	3.4e-18			74.03	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1356	1cdy		135	315	6.3e-23	0.35	0.64		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1356	1ce1	L	22	222	1.2e-21			72.17	CAMPATH-1H; LIGHT CHAIN; CHAIN: L;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	
1356	1cs6	A	26	395	1.7e-58	0.23	0.55		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1356	1cvs	C	122	315	1.2e-42	0.32	0.52		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	C	240	395	1.7e-35	0.07	-0.18		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	C	29	120	6.8e-13	-0.07	0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	C	34	223	1.4e-28	0.03	0.10		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	122	315	1.2e-42	0.28	0.47		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	240	395	3.4e-37	0.16	-0.14		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	29	120	1e-11	-0.14	0.33		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1cvs	D	34	223	1e-26	-0.12	0.37		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1356	1d5i	L	29	222	3.4e-22	-0.08	0.65		CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
1356	1dee	A	29	222	1.4e-22	0.10	0.43		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H; IMMUNOGLOBULIN 3D6 FAB 1DFB 3	2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
1356	1dfb	L	22	222	1.2e-21			76.72		
1356	1dgi	R	29	315	5.1e-43	-0.29	0.27		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS- RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1356	1epf	A	118	305	4.2e-28	0.47	0.63		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1epf	A	128	299	5.1e-22	0.34	1.00		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1epf	A	235	379	1.7e-21	0.05	-0.09		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1epf	A	27	225	5.1e-26	0.25	0.11		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1356	1ev2	E	123	315	6.8e-39	-0.11	0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev2	E	240	395	1.5e-33	0.06	-0.17		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG)LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev2	E	34	223	6.8e-24	0.24	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev2	G	123	319	8.5e-43	0.29	0.23		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev2	G	240	395	1.7e-36	0.10	-0.07		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev2	G	29	124	1.7e-11	-0.03	0.24		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev2	G	34	223	1e-24	0.14	0.42		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1ev1	C	122	315	1.7e-41	0.23	0.39		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1evt	C	29	120	1.7e-11	-0.08	0.10		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFI; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1evt	C	34	223	5.1e-25	-0.07	0.22		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFI; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1356	1f2q	A	119	318	2.1e-19	0.18	0.35		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1356	1fcg	A	123	315	6.3e-23	0.23	0.55		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1356	1fcg	A	228	395	3.4e-18	0.02	-0.19		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1356	1fhg	A	225	315	8.5e-18	0.25	0.94		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1356	1fhg	A	31	120	3.4e-14	0.14	0.30		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1356	1fvd	A	22	222	3.4e-22			73.26	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	BARREL
1356	1fvd	A	29	222	3.4e-22	0.12	0.55		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1356	1gc1	L	22	222	3.4e-21			73.99	ENVELOPE PROTEIN GP120; CHAIN: G; CD4; CHAIN: C; ANTIBODY 17B; CHAIN: L, H;	COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB) COMPLEX (HIV ENVELOPE PROTEIN/CD4/FAB), HIV-1 EXTERIOR 2 ENVELOPE GP120, T-CELL SURFACE GLYCOPROTEIN CD4, 3 ANTIGEN-BINDING FRAGMENT OF HUMAN IMMUNOGLOBULIN 17B, 4 GLYCOSYLATED PROTEIN
1356	1hng	A	135	317	4.2e-26	0.32	0.03		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAV) IHNG 3	
1356	1igt	B	23	393	1e-18			74.95	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1356	1ith	B	145	393	5.1e-19	-0.07	0.09		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1356	1ith	B	32	319	2.1e-24			81.96	INTERLEUKIN-1 BETA;	COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	(IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1356	1ibb	B	34	315	2.1e-24	0.04	0.06		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1356	1koa		26	120	1.7e-11	-0.35	0.12		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1356	1ihl	A	28	219	1.7e-25	0.24	0.98		LAMBDA III BENGE JONES PROTEIN CLE; CHAIN: A, B	IMMUNOGLOBULIN IMMUNOGLOBULIN, BENGE JONES PROTEIN
1356	1mco	H	10	395	8.5e-25			83.75	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1356	1mco	H	25	384	8.5e-25	-0.18	0.33		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (GG1) (MCG) WITH A HINGE DELETION IMCO 3	
1356	1nct		226	315	1.1e-17	0.40	0.16		TTTN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1356	Inct		29	121	1.5e-14	0.11	0.05		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1356	Infd	E	27	220	5.1e-25	0.38	0.74		N15 ALPHA-BETA T-CELL RECEPTOR; CHAIN: A, B, C, D; H57 FAB; CHAIN: E, F, G, H	COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN) COMPLEX (IMMUNORECEPTOR/IMMUNOGLOBULIN)
1356	Iosp	L	22	222	1.7e-16			76.74	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSP A; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1, BORRELLIA BURGDORFERI 3 STRAIN B31
1356	Itmm		29	121	1.5e-14	-0.03	0.18		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	
1356	2fcb	A	228	395	3.4e-18	0.01	-0.18		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1356	2fcb	A	28	191	8.5e-14	-0.28	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1356	2fgw	L	29	222	5.1e-23	-0.07	0.29		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1356	2ncm		27	120	3.4e-12	0.21	0.36		OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-O2.FAB) 2FGW 4	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1356	3fct	A	22	222	1.7e-21			77.52	METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
1356	8fab	A	26	221	8.5e-29			73.89	IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1356	8fab	A	28	219	8.5e-29	0.18	0.94		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1367	1b1i	A	29	129	4.2e-30	-0.05	0.76		HYDROLASE ANGIOGENIN; CHAIN: A;	HYDROLASE HYDROLASE (VASCULARIZATION)
1367	1b6v	A	21	132	1.7e-43			50.95	RIBONUCLEASE; CHAIN: A, B;	MOLECULAR EVOLUTION MOLECULAR EVOLUTION, RIBONUCLEASE
1367	1b6v	A	27	132	1.7e-43	-0.27	0.98		RIBONUCLEASE; CHAIN:	MOLECULAR EVOLUTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1367	1bsr	A	27	132	5.1e-42	-0.47	0.66		A, B;	MOLECULAR EVOLUTION, RIBONUCLEASE
									HYDROLASE(PHOSPHO RIC DIESTER,RNA) RIBONUCLEASE (BOVINE, SEMINAL) (BS-RNASE) 1BSR 3	
1367	1dy5	A	27	132	3.4e-44	0.16	0.93		RIBONUCLEASE A; CHAIN: A, B;	HYDROLASE (PHOSPHORIC DIESTER) RIBONUCLEASE, DEAMIDATION, ULTRA-HIGH RESOLUTION
1367	1qnt	A	24	132	3.4e-41	-0.11	1.00		EOSINOPHIL CATIONIC PROTEIN; CHAIN: A;	RIBONUCLEASE RIBONUCLEASE 3, RNASE 3 EOSINOPHIL, RIBONUCLEASE, CYTOTOXICITY
1367	1rbd		41	132	1.7e-39	-0.51	0.88		HYDROLASE(PHOSPHO RIC DIESTER,RNA) RIBONUCLEASE S (E.C.3.1.27.5) MUTANT WITH MET 13 REPLACED BY 1RBD 3 ALPHA-AMINO-NORMAL-BUTYRIC ACID (M13ABA) 1RBD 4	
1367	1rnf	A	31	130	3.4e-34	0.10	0.96		RIBONUCLEASE 4; CHAIN: A, B;	HYDROLASE RNASE 4; HYDROLASE, RIBONUCLEASE, PHOSPHODIESTERASE
1367	1rnu		27	132	8.5e-45	-0.13	0.93		HYDROLASE(PHOSPHO RIC DIESTER,RNA) RIBONUCLEASE S (E.C.3.1.27.5) (PH 5.5) 1RNU 3	
1367	1rra	A	28	132	1.7e-41	0.00	0.96		RIBONUCLEASE; CHAIN: A;	HYDROLASE RNASE A; HYDROLASE(PHOSPHORIC DIESTER), RIBONUCLEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1367	1strn	A	27	114	1.7e-39	-0.20	0.90		HYDROLASE (NUCLEIC ACID,RNA) SEMISYNTHETIC RIBONUCLEASE A (R* NASE 1-118(COLON)111-124) ISRN 3 (E.C.3.1.27.5) ISRNA 1 ISRNA 2	
1388	1awq	A	42	193	1.7e-75			166.81	CYCLOPHILIN A; CHAIN: A; PEPTIDE FROM THE HIV-1 CAPSID PROTEIN; CHAIN: B;	COMPLEX (ISOMERASE/PEPTIDE) COMPLEX (ISOMERASE/PEPTIDE), CYCLOPHILIN A, HIV-1 CAPSID, 2 PSEUDO-SYMMETRY
1388	1cyn	A	39	194	3.4e-65			225.00	CYCLOPHILIN B; ICYN 6 CHAIN: A; ICYN 7 (D-(CHOLINYL)AL A)8- CYCLOSPORIN; ICYN 10 CHAIN: C; ICYN 11	COMPLEX (ISOMERASE/IMMUNOSUPPRESS ANT) CYCLOSPORIN, ISOMERASE, ROTAMASE, SIGNAL, ICYN 19
1392	1tal		28	112	0.006	0.84	0.19		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1393	1l88	A	101	168	3.4e-06	-0.92	0.01		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT
1423	1b6v	A	32	133	8.5e-49	0.31	1.00		RIBONUCLEASE; CHAIN: A, B;	MOLECULAR EVOLUTION MOLECULAR EVOLUTION, RIBONUCLEASE
1423	1b6v	A	32	148	8.5e-49			77.74	RIBONUCLEASE; CHAIN: A, B;	MOLECULAR EVOLUTION MOLECULAR EVOLUTION, RIBONUCLEASE
1423	1bst	A	32	133	1e-47	0.01	0.87		HYDROLASE/PHOSPHO	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RIC DIESTER, RNA) RIBONUCLEASE (BOVINE, SEMINAL) (BS- RNASE) IBSR 3	
1423	1bsr	A	32	148	1e-47			66.58	HYDROLASE(PHOSPHO RIC DIESTER, RNA) RIBONUCLEASE (BOVINE, SEMINAL) (BS- RNASE) IBSR 3	
									RIBONUCLEASE A; CHAIN: A, B;	HYDROLASE (PHOSPHORIC DIESTER) RIBONUCLEASE, DEAMIDATION, ULTRA-HIGH RESOLUTION
1423	1dy5	A	32	133	5.1e-47	0.38	1.00		EOSINOPHIL CATIONIC PROTEIN; CHAIN: A;	RIBONUCLEASE RIBONUCLEASE 3, RNASE 3 EOSINOPHIL, RIBONUCLEASE, CYTOTOXICITY
1423	1qnt	A	30	133	3.4e-36	0.29	1.00		HYDROLASE(PHOSPHO RIC DIESTER, RNA) RIBONUCLEASE S (E.C.3.1.27.5) MUTANT WITH MET 13 REPLACED BY IRBD 3 ALPHA-AMINO- NORMAL-BUTYRIC ACID (M13ABA) IRBD 4	
1423	1rbd		46	133	8.5e-44	0.51	0.96		HYDROLASE(PHOSPHO RIC DIESTER, RNA) RIBONUCLEASE S (E.C.3.1.27.5) MUTANT WITH MET 13 REPLACED BY IRBD 3 ALPHA-AMINO- NORMAL-BUTYRIC ACID (M13ABA) IRBD 4	
1423	1rbd		46	148	8.5e-44			77.31	HYDROLASE(PHOSPHO RIC DIESTER, RNA) RIBONUCLEASE S (E.C.3.1.27.5) MUTANT WITH MET 13 REPLACED BY IRBD 3 ALPHA-AMINO- NORMAL-BUTYRIC ACID (M13ABA) IRBD 4	
1423	1mf	A	32	133	1.7e-35	0.36	0.95		RIBONUCLEASE 4;	HYDROLASE RNASE 4;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	HYDROLASE, RIBONUCLEASE, PHOSPHODIESTERASE
1423	1rmf	A	33	152	1.7e-35			58.15	RIBONUCLEASE 4; CHAIN: A, B;	HYDROLASE RNASE 4; HYDROLASE, RIBONUCLEASE, PHOSPHODIESTERASE
1423	1rmu		32	133	3.4e-49	0.36	0.99		HYDROLASE(PHOSPHO RIC DIESTER, RNA) RIBONUCLEASE S (E.C.3.1.27.5) (PH 5.5) 1RNU 3	
1423	1rmu		32	148	3.4e-49			79.09	HYDROLASE(PHOSPHO RIC DIESTER, RNA) RIBONUCLEASE S (E.C.3.1.27.5) (PH 5.5) 1RNU 3	
1423	1rra	A	33	133	5.1e-45	0.04	0.99		RIBONUCLEASE; CHAIN: A;	HYDROLASE RNASE A; HYDROLASE(PHOSPHORIC DIESTER), RIBONUCLEASE
1423	1srn	A	32	133	3.4e-49	0.25	0.99		HYDROLASE (NUCLEIC ACID, RNA) SEMISYNTHETIC RIBONUCLEASE A (R*NASE 1- 118(COLON)111-124) ISRN 3 (E.C.3.1.27.5) ISRNA 1 ISRNA 2	
1423	1srn	A	32	134	3.4e-49			80.10	HYDROLASE (NUCLEIC ACID, RNA) SEMISYNTHETIC RIBONUCLEASE A (R*NASE 1- 118(COLON)111-124) ISRN 3 (E.C.3.1.27.5) ISRNA 1 ISRNA 2	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1a4y	A	1	166	4e-20	0.16	-0.01		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1427	1a9n	A	1	129	6e-21	0.41	0.64		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1427	1a9n	A	1	63	0.00017	0.07	0.63		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1427	1a9n	A	33	179	4e-20	0.62	0.47		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1427	1a9n	C	1	135	4e-21	0.40	0.37		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1427	1a9n	C	33	179	8e-20	0.51	0.78		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1427	1b1h	A	210	330	4e-10	0.44	0.11		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1427	1b1v		339	424	0.0015	-0.02	0.07		TTTN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1cs6	A	166	298	1.7e-10	-0.17	0.22		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1427	1cs6	A	210	342	4e-13	0.27	0.24		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1427	1evs	C	229	360	1.4e-06	0.15	0.16		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1427	1evs	D	211	299	1e-16	0.50	0.62		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1427	1evs	D	229	350	5.1e-06	0.24	0.10		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1427	1d0b	A	1	154	3.4e-22	0.61	0.96		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1427	1dce	A	1	115	4e-14	0.37	0.86		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1dce	A	29	135	8.5e-10	0.45	1.00		SUBUNIT; CHAIN: B, D; RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1427	1ds9	A	7	140	1.2e-18	0.22	0.65		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1427	1ev2	G	207	302	2e-17	0.57	0.37		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1427	1ev2	G	222	342	2e-14	0.32	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1427	1evt	C	222	342	2e-14	0.34	0.35		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1427	1fhg	A	205	301	1.8e-18	0.38	0.59		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1fhh	A	154	422	4e-07			72.40	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	241	419	4e-07	0.37	0.33		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	318	416	6.8e-06	-0.42	0.43		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1fhh	A	340	442	0.00014	0.05	0.39		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1427	1foi	A	24	65	6.8e-05	-0.44	0.51		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1foi	A	2	62	1.7e-05	0.02	0.23		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1foi	B	24	65	6.8e-05	-0.49	0.43		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1foi	B	2	62	1.7e-05	0.15	0.76		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1427	1fqv	A	1	146	1.4e-11	0.09	-0.12		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDC2-ASSOCIATED PROTEIN P45; CYCLIN A/CDC2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1fs2	A	1	135	4e-16	0.17	-0.05		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	PROTEIN LIGASE LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRKS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1427	1mfn		333	419	2e-07	0.01	0.28		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1427	1mfn		341	416	1e-06	-0.03	0.53		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1427	1nct		209	298	1e-19	0.43	0.92		TTIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1427	1qr4	A	230	415	6e-08	0.34	-0.12		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1427	1ten		339	419	8e-07	-0.44	0.11		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	
1427	1tmn		213	298	6e-18	0.64	0.65		MUSCLE PROTEIN TTIN	

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1427	1wio	A	211	364	2e-15	0.19	0.21		MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1427	1wit		210	298	8e-19	0.50	0.31		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1427	1wvc	A	209	303	6e-21	0.20	0.15		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, 1 SET, MUSCLE PROTEIN
1427	1wvw	X	215	302	1.4e-16	0.05	0.04		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1427	1yrg	A	2	166	1e-16	0.19	-0.09		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2 IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1427	2buh		1	170	4e-25	0.28	0.29		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPL, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY ACETYLATION RNASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									INHIBITOR; CHAIN: NULL;	INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1427	2bnh		2	323	1.7e-14	0.31	-0.07		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1427	2ncm		210	298	4e-16	0.29	0.70		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN I; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1427	3ncm	A	211	298	4e-18	0.52	0.48		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1437	1dan	L	897	980	1.7e-11	0.01	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DEFRCKM) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1437	1dva	L	897	980	1.7e-11	0.06	-0.19		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL ID score	Compound	PDB annotation
1437	1dx5	I	703	808	5.1e-12	0.11	-0.20		VILA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	
1437	1dx5	I	703	808	5.1e-12	0.11	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1437	1enn		652	729	5.1e-08	0.32	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1437	1enn		703	767	6.8e-09	0.28	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1437	1enn		817	884	3.4e-09	0.04	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1437	1ezg	A	669	758	3.4e-08	0.20	-0.19		THERMAL HYSTERESIS PROTEIN ISOFORM YL-1; CHAIN: A, B;	DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILIN-1 FRAGMENT, MATRIX PROTEIN
1437	1fak	L	897	980	1.7e-11	0.16	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: L;	ANTIFREEZE PROTEIN INSECT ANTIFREEZE PROTEIN, THERMAL HYSTERESIS, TENEBRIO 2 MOLITOR, IODINATION, RIGHT-HANDED BETA-HELIX, TMAFP
1437	1fak	L	897	980	1.7e-11	0.16	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: L;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1437	1klo		509	683	1.5e-08	0.18	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1klo		580	735	1.7e-09	0.06	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1klo		780	921	1.7e-13	0.02	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1klo		824	989	3.4e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1klo		876	1036	3.4e-20	0.01	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1437	1pfx	L	523	618	5.1e-09	0.11	-0.20		FACTOR IXA; CHAIN: C; I ₂ ; D-PHE-PRO-ARG; CHAIN: L;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1437	1qfk	L	901	980	8.5e-11	0.36	-0.17		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;	SERINE PROTEASE FVIA; FVIA; BLOOD COAGULATION, SERINE PROTEASE

Table 5

SEQ ID No:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									COAGULATION FACTOR VIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	
1437	1vmo	A	570	741	4.4e-31	0.49	-0.12		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 IVMO 3	
1437	1vmo	A	637	800	4.4e-26	0.78	-0.15		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 IVMO 3	
1437	1vmo	A	687	878	1.3e-23	0.13	-0.18		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 IVMO 3	
1437	1vmo	A	721	935	8.8e-22	0.23	-0.19		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 IVMO 3	
1437	1vmo	A	819	985	6.6e-26	0.34	-0.19		MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN 1 IVMO 3	
1437	1xka	L	777	861	1.7e-10	0.02	-0.20		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1437	9wga	A	548	723	3.4e-12	0.27	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1437	9wga	A	601	775	8.5e-15	0.02	-0.19		LECTIN (AGGLUTININ)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1437	9wga	A	647	816	8.5e-13	0.25	-0.19		WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1437	9wga	A	734	918	1.7e-11	-0.00	-0.20		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1437	9wga	A	765	963	1.2e-14	0.13	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1437	9wga	A	822	990	5.1e-13	0.05	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1437	9wga	A	848	1016	5.1e-15	0.22	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1442	1a4y	A	56	242	1.5e-15	0.11	0.28		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPI TOPE MAPPING, LEUCINE-RICH 3 REPEATS
1442	1a9n	A	59	145	4.4e-09	-0.04	0.47		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C, U2 B";	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1442	1a9n	A	66	187	1.5e-22	0.46	1.00		CHAIN: B, D; U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1442	1a9n	C	59	158	6.6e-10	0.18	0.63		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1442	1a9n	C	66	187	6.6e-22	0.17	0.98		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1442	1a9n	C	89	200	1.8e-16	0.43	0.16		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1442	1d0b	A	36	163	5.1e-21	0.67	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1442	1d0b	A	39	186	8.8e-15	0.23	-0.07		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1442	1dce	A	38	140	3.4e-10	0.73	0.89		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1442	1dce	A	57	163	6.8e-12	0.12	0.93		RAB GERANYLGERANYLTRANSFERASE ALPHA	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D; OUTER ARM DYNEIN; CHAIN: A;	E, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1442	1ds9	A	47	162	1.7e-11	-0.02	0.84		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1442	1fqv	A	35	162	6.8e-08	0.42	0.17		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1442	1fs2	A	35	162	6.8e-08	0.23	0.22		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1442	1yrg	A	59	186	8.8e-14	-0.06	0.63		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMISPHERAL TWINNING, 3 MEROPEDRAL TWINNING, MEROPEDRY ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN
1442	2bnh		56	266	1.3e-16	0.06	-0.05		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1442	2bnh		59	192	6.6e-20	-0.05	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1443	1aab		2	81	1e-27			73.20	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1443	1aab		3	75	1e-27	0.34	1.00		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1443	1aab		83	123	1.5e-07	-0.51	0.17		HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	DNA-BINDING HMGA DNA-BINDING HMG-BOX DOMAIN A OF RAT HMGI; 1AAB 8 HMG-BOX 1AAB 20
1443	1cct	A	5	75	6.8e-27	0.11	1.00		HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(IDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMGI-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1443	1cct	A	5	75	6.8e-27			65.26	HIGH MOBILITY GROUP 1 PROTEIN; CHAIN: A; DNA (5'-D(*CP*CP*(IDO) CHAIN: B; DNA (5'-CHAIN: C;	GENE REGULATION/DNA HMGI-1, AMPHOTERIN, HEPARIN-BINDING PROTEIN P30; HIGH-MOBILITY GROUP DOMAIN, BENT DNA, PROTEIN-DRUG-DNA 2 COMPLEX, GENE REGULATION/DNA
1443	1hne		91	159	3.4e-10	-0.49	0.11		DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									(HMG1) (DNA-BINDING HME 3 HMG-BOX DOMAIN B OF RAT HMG1) (NMR, 1 STRUCTURE) 1HME 4	
1443	1hsm		91	163	5.1e-11	-0.42	0.42		DNA-BINDING HIGH MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED WITH 1HSM 3 MERCAPTOETHANOL (NMR, MINIMIZED AVERAGE STRUCTURE) 1HSM 4	
1443	1qrv	A	88	123	1.1e-08	-0.86	0.22		DNA (5'- D*Gp* Cp*Gp*Ap*Tp*Ap *Tp* Cp*Gp*C)-3'); CHAIN: C, D; HIGH MOBILITY GROUP PROTEIN D; CHAIN: A, B;	GENE REGULATION/DNA HMG-D; PROTEIN-DNA COMPLEX, HMG DOMAIN, NON-SEQUENCE SPECIFIC 2 CHROMOSOMAL PROTEIN HMG-D
1477	1mey	C	232	316	1.4e-35	-0.63	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1477	1ubd	C	214	316	9.8e-29	-0.76	0.16		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1482	1ctq	A	447	482	1.2e-06	-0.54	0.10		TRANSFORMING PROTEIN P21/H-RAS-1;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1482	1dpt	A	400	482	6e-07	0.05	0.10		CHAIN: A; RHOA; CHAIN: A;	CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN GENE REGULATION/SIGNALING PROTEIN RHOA-GDP COMPLEX
1482	1huq	A	443	482	3.6e-07	-0.88	0.41		RAB5C; CHAIN: A;	PROTEIN TRANSPORT G- PROTEIN, GTP HYDROLYSIS, ENDOCYTOSIS, RAB PROTEIN, 2 MEMBRANE TRAFFICKING
1484	1buo	A	71	190	8.4e-16	-0.01	0.21		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION REVERSE TRANSCRIPTASE
1487	1mm1		395	507	0.0018	-0.46	0.09		MM1V REVERSE TRANSCRIPTASE, 1MM1, 4 CHAIN: NULL; 1MM1 5	
1489	1fgx	A	104	403	0	0.67	1.00		BETA 1,4 GALACTOSYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE BETA4GAL'T1; NUCLEOTIDE BINDING PROTEIN, ALPHA BETA ALPHA FOLD
1489	1fgx	A	94	404	0			343.91	BETA 1,4 GALACTOSYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE BETA4GAL'T1; NUCLEOTIDE BINDING PROTEIN, ALPHA BETA ALPHA FOLD
1491	1clg	A	22	301	4.2e-10			61.55	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1491	1dgt	A	23	145	7e-31	-0.19	0.90		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE-BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1491	1f5n	A	23	145	7e-31	-0.39	0.92		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1491	1i1i	P	25	273	7.2e-09	-0.34	0.01		NEUROLYSIN; CHAIN: P;	HYDROLASE NEUROPEPTIDASE, ZINC METALLOPEPTIDASE, ENDOPEPTIDASE
1493	1g0s	A	297	396	3.6e-07	-0.10	0.00		HYPOTHETICAL 23.7 KDA PROTEIN IN ICC-TOLC CHAIN: A, B;	HYDROLASE ADP-RIBOSE PYROPHOSPHATASE, NUDIX FOLD
1497	1b0w	A	1	95	7e-57			113.54	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
1497	1b0w	A	23	125	2.4e-63			123.78	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
1497	1b6d	A	23	124	5.6e-65	0.86	1.00		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN
1497	1b1l	J	23	124	2.8e-66	0.85	1.00		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1497	1bvk	A	1	95	2.8e-56			113.70	HULYSII; CHAIN: A, B, D, E, LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE, HUMANIZED

Table 5

SEQ ID NO:	PDB ID	CHAIN NID	STAR T AA	END AA	Psi Blast	Verity score	PMF score	SEQFOL D score	Compound	PDB annotation
1497	1bvk	A	23	119	1.2e-63	0.95	1.00		HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1497	1bvk	A	23	125	1.2e-63			123.99	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE: HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1497	1bw	A	1	95	8.4e-59			116.30	IG KAPPA CHAIN V-I REGION REL; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENGE-JONES 2 PROTEIN, IMMUNE SYSTEM
1497	1bw	A	21	125	2.8e-65			127.42	IG KAPPA CHAIN V-I REGION REL; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENGE-JONES 2 PROTEIN, IMMUNE SYSTEM
1497	1bw	A	23	124	2.8e-65	0.85	1.00		IG KAPPA CHAIN V-I REGION REL; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENGE-JONES 2 PROTEIN, IMMUNE SYSTEM
1497	1dee	A	23	124	7e-68	1.07	1.00		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A;	IMMUNE SYSTEM FAB-1BP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1497	1dql	L	1	95	5.6e-57			111.65	CHAIN: G, H; IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	FAB VH3 3 SPECIFICITY IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
1497	1dql	L	23	125	7e-63			123.32	IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
1497	1fgv	L	1	93	1.4e-60			121.32	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1497	1fgv	L	23	124	4.2e-66	0.97	1.00		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1497	1fgv	L	23	125	4.2e-66			131.86	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1497	1fvc	A	1	95	1.1e-57			115.15	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3 IMMUNOGLOBULIN FV	
1497	1fvc	A	23	124	5.6e-64	0.82	1.00			

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
1497	1fvc	A	23	125	5.6e-64			125.91	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
1497	1fvd	A	23	124	2.8e-64	1.00	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1497	1igm	L	1	93	8.4e-59			113.29	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
1497	1igm	L	23	124	4.2e-64	0.86	1.00		IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
1497	1igm	L	23	125	4.2e-64			123.98	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
1497	1wtl	A	1	93	4.2e-57			116.77	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
1497	1wtl	A	23	125	1.2e-63			127.46	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL ID score	Compound	PDB annotation
									LIGHT-CHAIN 1 WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
1497	2fgw	L	23	124	7e-67	0.94	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
1498	1a80		104	367	5.6e-69	0.12	0.99		2,5-DIKETO-D-GLUCONIC ACID REDUCTASE A; CHAIN: NULL;	OXIDOREDUCTASE 2,5-DKG REDUCTASE A; OXIDOREDUCTASE, ALPHA8/BETA8 BARREL, 2,5-DIKETO-D-GLUCONIC 2 ACID, COMMERCIAL VITAMIN C SYNTHESIS
1498	1a80		122	372	5.6e-69			62.58	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE A; CHAIN: NULL;	OXIDOREDUCTASE 2,5-DKG REDUCTASE A; OXIDOREDUCTASE, ALPHA8/BETA8 BARREL, 2,5-DIKETO-D-GLUCONIC 2 ACID, COMMERCIAL VITAMIN C SYNTHESIS
1498	1ads		105	365	2.8e-84	0.05	0.96		OXIDOREDUCTASE ALDOSE REDUCTASE (E.C.1.1.1.21) COMPLEX WITH NADPH 1ADS 3	
1498	1ads		82	372	2.8e-84			105.14	OXIDOREDUCTASE ALDOSE REDUCTASE (E.C.1.1.1.21) COMPLEX WITH NADPH 1ADS 3	
1498	1afs	A	68	372	1.1e-72			101.13	3-ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA-HSD; OXIDOREDUCTASE, NAD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1498	1afs	A	99	368	1.1e-72	0.16	0.83		3-ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA-HSD; OXIDOREDUCTASE, NAD
1498	1ah4		105	365	1.1e-83	-0.09	0.94		ALDOSE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1ah4		81	372	1.1e-83			103.47	ALDOSE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE, ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1c9w	A	105	365	2.8e-81	0.12	0.84		CHO REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ALPHA/BETA TIM BARREL, PROTEIN-NADP+ COMPLEX
1498	1c9w	A	80	372	2.8e-81			103.01	CHO REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ALPHA/BETA TIM BARREL, PROTEIN-NADP+ COMPLEX
1498	1cwn		106	368	9.8e-78	0.09	0.70		ALDEHYDE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE ALR1; TIM-BARREL, OXIDOREDUCTASE, NADP
1498	1cwn		79	372	9.8e-78			81.73	ALDEHYDE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE ALR1; TIM-BARREL, OXIDOREDUCTASE, NADP
1498	1ei3	A	102	365	2.8e-85	0.21	0.99		ALDOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1ei3	A	82	372	2.8e-85			106.54	ALDOSE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE ALDOSE REDUCTASE, INHIBITION, DIABETES
1498	1ftb		105	365	1.4e-80	0.08	0.90		FR-1 PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE (NADP) ALDO-KETO OXIDOREDUCTASE (NADP), TIM BARREL
1498	1ftb		80	372	1.4e-80			98.60	FR-1 PROTEIN; CHAIN: NULL;	OXIDOREDUCTASE (NADP)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1498	1hw6	A	104	367	1.4e-66	0.15	0.90		NULL;	ALDO-KETO OXIDOREDUCTASE (NADP), TIM BARREL
									2,5-DIKETO-D-GLUCONIC ACID REDUCTASE; CHAIN: A;	OXIDOREDUCTASE APO-2,5-DIKETO-D-GLUCONATE REDUCTASE; ALDO-KETO REDUCTASE, TIM BARREL
1498	1hw6	A	113	365	1.4e-66			67.97	2,5-DIKETO-D-GLUCONIC ACID REDUCTASE; CHAIN: A;	OXIDOREDUCTASE APO-2,5-DIKETO-D-GLUCONATE REDUCTASE; ALDO-KETO REDUCTASE, TIM BARREL
1498	2alr		106	368	1.1e-76	0.22	0.70		ALDEHYDE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE ALR1; OXIDOREDUCTASE, TIM-BARREL
1498	2alr		79	372	1.1e-76			61.33	ALDEHYDE REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE ALR1; OXIDOREDUCTASE, TIM-BARREL
1499	1flm	A	543	626	1.2e-18	0.33	-0.18		OUTER SURFACE PROTEIN C; CHAIN: A, B, C, D;	IMMUNE SYSTEM OSPC; LYME DISEASE, OSPC, HB19, HELICAL BUNDLE, DIMER
1499	1flm	A	550	626	3.6e-17	0.14	-0.15		OUTER SURFACE PROTEIN C; CHAIN: A, B, C, D;	IMMUNE SYSTEM OSPC; LYME DISEASE, OSPC, HB19, HELICAL BUNDLE, DIMER
1499	1flm	A	551	626	9.6e-17	0.32	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A, B, C, D;	IMMUNE SYSTEM OSPC; LYME DISEASE, OSPC, HB19, HELICAL BUNDLE, DIMER
1499	1g5z	A	550	626	1.2e-17	0.36	-0.19		OUTER SURFACE PROTEIN C; CHAIN: A;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	550	626	3.6e-17	0.04	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	551	626	1.2e-17	0.34	-0.19		OUTER SURFACE PROTEIN C; CHAIN: A;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	551	626	1.2e-17	0.52	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1499	1g5z	A	551	626	2.4e-17	0.18	-0.19		OUTER SURFACE	IMMUNE SYSTEM SURFACE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1499	1g5z	A	551	626	3.6e-17	0.67	-0.19		PROTEIN C; CHAIN: A; OUTER SURFACE	PROTEIN, ALPHA HELIX PROTEIN
1504	1ckl	A	10	79	1.4e-30			90.17	PROTEIN C; CHAIN: A; CD46; CHAIN: A, B, C, D, E, F;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1504	1ckl	A	1	72	2.8e-24			89.35	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1504	1ckl	A	222	347	1.4e-27			222.13	CD46; CHAIN: A, B, C, D, E, F;	GLYCOPROTEIN MEMBRANE COFACTOR PROTEIN (MCP); VIRUS RECEPTOR, COMPLEMENT COFACTOR, SHORT CONSENSUS REPEAT, 2 SCR, MEASLES VIRUS, GLYCOPROTEIN
1504	1g40	A	77	344	7e-35			81.51	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B;	IMMUNE SYSTEM BETA, MODULE
1504	1g44	A	166	406	5.6e-31			69.90	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1504	1g44	B	220	406	1.4e-25			74.78	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1504	1g44	C	153	406	5.6e-24			69.94	COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1504	1qub	A	74	406	4.2e-28			74.76	HUMAN BETA2-	MEMBRANE ADHESION SHORT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GLYCOPROTEIN I; CHAIN: A;	CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1511	1alh	A	281	363	4.2e-29	-0.50	0.03		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1511	1alh	A	367	436	2.8e-26	-0.33	0.28		QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1511	1bbo		369	424	4.2e-14	-0.42	0.42		DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 111BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO 4	
1511	1mey	C	10	73	1.4e-40			64.91	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mey	C	280	363	2.8e-47	-0.07	0.39		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mey	C	309	391	2.8e-49	-0.12	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID No:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mev	C	338	421	2.8e-49	0.17	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mev	C	338	424	2.8e-49			83.28	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mev	C	366	437	2.8e-40	-0.25	0.15		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1mev	G	336	363	5.6e-13	0.73	0.99		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1511	1tf6	A	235	400	1.4e-35	-0.57	0.33		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1511	1tf6	A	279	449	1.4e-35			65.99	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1511	1tt6	A	339	447	4.2e-24	-0.51	0.06		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1511	1ubd	C	309	420	6e-35			68.77	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	1ubd	C	314	419	1.4e-34	-0.02	0.87		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	1ubd	C	324	403	6e-35	-0.34	0.37		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	1ubd	C	346	436	4.2e-28	-0.08	0.15		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION REGULATION/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1511	2gli	A	288	421	2.8e-33	-0.30	0.22		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1511	2gli	A	309	449	2.8e-33			63.97	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1511	2gli	A	317	435	7e-31	0.05	0.77		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1511	2gli	A	346	446	1.1e-22	0.09	-0.15		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1513	1hi7	A	139	173	0.0015	-0.26	0.06		PS2 PROTEIN; CHAIN: A, B;	GROWTH FACTOR PNR-2, PS2, TF1, BREAST CANCER ESTROGEN INDUCIBLE GROWTH FACTOR, CELL MOTILITY, TUMOR SUPPRESSOR, TRF01.2 DOMAIN, SIGNAL
1518	1bm6		21	116	1.4e-34			131.75	BETA=2--MICROGLOBULIN; 1BMG 5 CHAIN: NULL 1BMG 6	HISTOCOMPATIBILITY ANTIGEN LACTOLIN, MHC-1 HISTOCOMPATIBILITY ANTIGEN, LIGHT CHAIN 1BMG 11
1518	1i4f	B	1	85	7e-31			134.89	HLA CLASS I	IMMUNE SYSTEM MAGE-4

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1518	1i4f	B	20	116	2.8e-34			157.82	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1521	1bmp		12	115	4.2e-49			156.36	BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
1521	1bmp		638	741	4.2e-50	0.36	1.00		BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
1521	1bmp		638	741	4.2e-50			156.52	BONE MORPHOGENETIC PROTEIN-7; CHAIN: NULL;	TRANSFORMING GROWTH FACTOR OSTEOGENIC PROTEIN-1, HOP-1, BMP-7; MORPHOGEN, TRANSFORMING GROWTH FACTOR, CYTOKINE, BONE, 2 CARTILAGE, GLYCOPROTEIN
1521	1poi	A	40	257	7e-39	0.29	0.62		GLUTACONATE COENZYME A-	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsI Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									TRANSFERASE; CHAIN: A, B, C, D;	FERMENTATION
1521	1poi	A	53	244	1.1e-51	0.22	0.21		GLUTACONATE COENZYME A-TRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN FERMENTATION
1521	1poi	B	270	490	3.6e-60	0.13	0.93		GLUTACONATE COENZYME A-TRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN FERMENTATION
1521	1poi	B	273	501	2.8e-34	0.01	0.83		GLUTACONATE COENZYME A-TRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, COA, GLUTAMATE, PROTEIN FERMENTATION
1523	1atl	A	221	422	4.2e-39	0.70	1.00		ATROLYSIN C; 1ATL 4 CHAIN: A, B, C, D; 1ATL 5	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM D; 1ATL 6
1523	1atl	A	223	422	1.2e-42	0.73	1.00		ATROLYSIN C; 1ATL 4 CHAIN: A, B, C, D; 1ATL 5	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM D; 1ATL 6
1523	1bkc	A	222	421	1.2e-43	-0.25	0.17		TUMOR NECROSIS FACTOR-ALPHA-CONVERTING ENZYME; CHAIN: A, C, E, I;	ZN-ENDOPEPTIDASE TACE; ZN-ENDOPEPTIDASE, HYDROLASE, TNF-ALPHA
1523	1bkc	A	225	417	9.8e-07	0.03	0.01		TUMOR NECROSIS FACTOR-ALPHA-CONVERTING ENZYME; CHAIN: A, C, E, I;	ZN-ENDOPEPTIDASE TACE; ZN-ENDOPEPTIDASE, HYDROLASE, TNF-ALPHA
1523	1bud	A	222	420	2.8e-36	0.65	0.87		ACUTOLYSIN A; CHAIN: A;	TOXIN HEMORRHAGIN I, 1AAH-I; METALLOPROTEINASE, SNAKE VENOM, MMP, TOXIN
1523	1dan	L	662	718	1.4e-07	0.34	0.23		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DIFFROMK) WITH CHAIN: C;	INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1523	1dva	L	662	718	1.4e-07	0.53	0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1523	1emn		589	656	2.8e-11	0.15	-0.17		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1523	1emn		629	690	1.4e-09	0.19	0.06		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1523	1emn		663	718	4.2e-07	0.40	-0.01		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1523	1fak	L	662	718	1.4e-07	0.64	0.25		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	DOMAIN, HUMAN FIBRILIN-1 FRAGMENT, MATRIX PROTEIN
1523	1fvl		439	508	4.2e-15	-0.04	0.84		FLAVORIDIN; 1FVL 4 CHAIN: NULL 1FVL 5	BLOOD COAGULATION INHIBITOR GP IIB/IIIA
1523	1fvl		439	512	1.2e-26	0.36	0.94		FLAVORIDIN; 1FVL 4 CHAIN: NULL 1FVL 5	BLOOD COAGULATION INHIBITOR GP IIB/IIIA
1523	1iag		221	422	2.8e-38	0.77	1.00		METALLOPROTEASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) IIAG 3	ANTAGONIST 1FVL 9
1523	1iag		223	422	4.8e-41	0.65	1.00		METALLOPROTEASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) IIAG 3	
1523	1igr	A	410	706	1.2e-11	0.15	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1523	1klo		461	630	7e-20	0.09	-0.13		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1523	1klo		519	664	2.8e-11	0.22	0.17		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1523	1klo		638	774	1.4e-10	0.07	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1523	1kst		439	508	1.3e-15	0.18	0.35		AGGREGATION INHIBITOR, GP	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTAGONIST KISTRIN (NMR, 8 STRUCTURES) IKST 3	
1523	1kst		439	510	3.6e-25	0.31	0.60		AGGREGATION INHIBITOR, GP ANTAGONIST KISTRIN (NMR, 8 STRUCTURES) IKST 3	
1523	1pfx	L	662	718	9.8e-08	0.53	0.72		FACTOR IXA; CHAIN: C ₁ ; D-PHE-PRO-ARG; CHAIN: I ₁	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1523	1qua	A	221	420	3.6e-39	0.63	1.00		ACUTOLYSIN-C; CHAIN: A ₁	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRODON ACUTUS
1523	1qua	A	221	420	9.8e-35	0.82	1.00		ACUTOLYSIN-C; CHAIN: A ₁	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRODON ACUTUS
1523	1qub	A	414	693	1.2e-11	0.01	-0.17		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A ₁	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1523	2ech		469	516	2.4e-18	-0.19	0.30		BLOOD COAGULATION	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									INHIBITOR ECHISTATIN (NMR, 8 STRUCTURES) 2ECH 3	
1523	9wga	A	502	666	2.8e-16	0.27	0.65		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1523	9wga	A	526	701	1.4e-12	0.09	0.23		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1523	9wga	A	661	859	7e-15	0.08	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1524	1alh	A	21	103	5.6e-31			75.55	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1524	1alh	A	2	84	4.2e-31			77.96	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1524	1alh	A	58	140	4.2e-31			77.62	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1524	1atl	A	8	210	1.4e-74			104.44	ATROLYSIN C; 1ATL 4	METALLOENDOPETIDASE

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Table 5

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B, C, D; 1ATL 5	HEMORRHAGIC TOXIN C, FORM D; 1ATL 6
1524	1bud	A	10	208	5.6e-71			97.67	ACUTOLYSIN A; CHAIN: A;	TOXIN HEMORRHAGIN 1, 1AAH-I; METALLOPROTEINASE, SNAKE VENOM, MMP, TOXIN
1524	1cfe		30	184	4.2e-42			82.74	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1524	1fv1		13	88	1.4e-25			67.46	FLAVORIDIN; 1FVL 4 CHAIN: NULL, 1FVL 5	BLOOD COAGULATION INHIBITOR GP IIB/IIIA
1524	1iag		7	210	4.2e-74			105.32	METALLOPROTEINASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) 1IAG 3	ANTAGONIST 1FVL 9
1524	1jln	A	21	247	2.8e-45	-0.00	-0.09		PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, R; CHAIN: A;	HYDROLASE STEP-LIKE PTPASE; PROTEIN-TYROSINE-PHOSPHATASE PROTEIN TYROSINE PHOSPHATASE, PTP-SL, PTPBR7, ERK2-MAP 2 KINASE REGULATION
1524	1kst		13	85	4.2e-25			66.02	AGGREGATION INHIBITOR, GP ANTAGONIST KISTRIN (NMR, 8 STRUCTURES) 1KST 3	
1524	1mey	C	1	64	2.8e-38			60.19	DNA: CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1524	1mey	C	1	66	1.1e-39			68.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	1mey	C	29	111	4.2e-50			93.01	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	1mey	C	48	130	2.8e-50			95.82	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	1mey	C	57	139	1.4e-50			95.58	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	1mey	C	57	139	2.8e-50			95.19	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1524	1mkp		100	242	1.2e-31			132.82	PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1524	1mkp		9	151	2.8e-34			133.40	PYST1; CHAIN: NULL;	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE
1524	1qnx	A	1	187	4.2e-44			81.43	VES V 5; CHAIN: A;	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
1524	1qua	A	7	208	7e-69			109.26	ACUTOLYSIN-C; CHAIN:	TOXIN HEMORRHAGIN III

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A;	METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRODON ACUTUS
1524	1trpm	A	18	241	2.8e-59	-0.04	0.35		RECEPTOR PROTEIN TYROSINE PHOSPHATASE MU; CHAIN: A, B;	RECEPTOR D1; RECEPTOR, PHOSPHATASE, SIGNAL TRANSDUCTION, ADHESION, 2 HYDROLASE
1524	1tf6	A	1	153	4.2e-37			71.61	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1tf6	A	1	153	5.6e-37			107.29	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1tf6	A	1	153	7e-38			101.40	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1tf6	A	3	144	8.4e-34			66.54	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1524	1ubd	C	1	111	4.2e-36			84.52	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1524	1ubd	C	20	130	5.6e-36			88.82	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1524	1ubd	C	31	139	2.8e-36			88.27	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1524	1ubd	C	3	111	1.4e-35			83.28	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1524	1vhr	A	81	250	2.4e-34			87.98	HUMAN VHL-RELATED	HYDROLASE VHR; HYDROLASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1524	lvhr	A	88	249	2.4e-34	0.36	1.00		DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1524	2gli	A	1	131	7e-33			76.01	HUMAN VH1-RELATED DUAL-SPECIFICITY PHOSPHATASE CHAIN: A, B;	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE
1524	2gli	A	1	140	2.8e-33			83.07	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1524	2gli	A	1	140	2.8e-33			88.13	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1524	2gli	A	1	140	7e-34			91.46	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1527	ldus	A	321	387	0.0036	0.18	0.34		MD0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1527	lg6q	1	293	382	0.00048	0.14	0.18		HNKRN ARGININE N-METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1528	laj4		52	207	5.6e-43	-0.34	0.15		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1528	1au1	B	245	399	1.3e-34	-0.11	0.00		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1528	1cdm	A	251	391	4.2e-53	-0.23	0.29		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1528	1cdm	A	324	415	4.2e-28	-0.18	0.11		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1528	1cll		251	391	5.6e-58	-0.39	0.40		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CELL 3	
1528	1cll		324	415	7e-29	0.03	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CELL 3	
1528	1cmf		322	391	1.4e-30	-0.09	0.59		CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1528	1dl	A	52	207	1.1e-39	-0.09	0.23		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1528	1exr	A	249	390	5.6e-56	0.10	0.05		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1528	1exr	A	320	415	9.8e-28	-0.09	0.16		CALMODULIN; CHAIN: A;	METAL TRANSPORT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A ₁	CALMODULIN, HIGH RESOLUTION, DISORDER
1528	1fw4	A	255	310	2.8e-15	0.09	-0.12		CALMODULIN; CHAIN: A ₁	METAL BINDING PROTEIN EF-HAND, HELIX-LOOP-HELIX, FRAGMENT, CALCIUM, TR2C, C-2 TERMINAL DOMAIN, CALMODULIN
1528	1fw4	A	327	390	9.8e-30	0.25	0.65		CALMODULIN; CHAIN: A ₁	METAL BINDING PROTEIN EF-HAND, HELIX-LOOP-HELIX, FRAGMENT, CALCIUM, TR2C, C-2 TERMINAL DOMAIN, CALMODULIN
1528	1g8i	A	234	386	2.8e-26	-0.23	0.07		NEURONAL CALCIUM SENSOR 1; CHAIN: A, B ₁	METAL BINDING PROTEIN FREQUENTIN; CALCIUM BINDING-PROTEIN, EF-HAND, CALCIUM ION
1528	1jfo	A	63	203	7e-17	-0.56	0.05		OBELIN; CHAIN: A ₁	LUMINESCENT PROTEIN BIOLUMINESCENCE, CALCIUM-REGULATED PHOTOPROTEIN, OBELIN, 2 OBELA, HYDROID
1528	1jf2	A	63	203	1.1e-16	-0.09	0.12		OBELIN; CHAIN: A ₁	LUMINESCENT PROTEIN BIOLUMINESCENCE, CALCIUM-REGULATED PHOTOPROTEIN, OBELIN, 2 OBELA, HYDROID
1528	1icf		245	391	4.2e-46	-0.14	0.51		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1528	1mx		251	390	4.2e-43	0.04	0.10		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMR score	SEQFOL D score	Compound	PDB annotation
1528	lmx		324	415	9.8e-26	-0.22	0.07		TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF-HAND ITNX 14
1528	ltop		251	393	9.8e-47	-0.07	0.11		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1528	ltop		324	415	9.8e-26	-0.41	0.15		CONTRACTILE SYSTEM PROTEIN TROPONIN C ITOP 3	
1528	lvrk	A	249	390	2.8e-56	-0.01	0.22		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1529	ldb3	A	153	449	4.2e-61	-0.31	0.05		GDP-MANNOSSE 4,6- DEHYDRATASE; CHAIN: A;	LYASE DEHYDRATASE, NADP, GDP-MANNOSSE, GDP-FUCOSE
1533	lal7		39	185	2.8e-13	0.07	-0.08		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER- HELIX, X-RAY STRUCTURE
1533	lal7		419	532	1.4e-18	0.48	0.12		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER- HELIX, X-RAY STRUCTURE
1533	lal7		9	134	4.2e-16	0.14	-0.12		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER- HELIX, X-RAY STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1533	1elr	A	184	284	1.1e-14	0.21	-0.02		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1elr	A	414	505	4.2e-15	0.34	0.25		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1elr	A	450	540	1.4e-13	0.36	0.30		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1elr	A	45	144	5.6e-11	0.14	0.06		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1533	1elw	A	184	300	7e-17	0.17	0.46		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1elw	A	423	524	4.2e-15	0.55	0.58		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1elw	A	42	154	9.8e-10	0.20	-0.17		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1elw	A	451	558	4.2e-15	0.58	0.07		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1elw	A	484	591	1.4e-15	0.02	-0.19		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE; CHAIN: C, D;	REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1elw	A	9	120	2.8e-15	0.18	-0.14		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1533	1feh	A	219	532	3.6e-11	0.14	0.58		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1533	1feh	A	319	598	1.3e-30	-0.00	-0.15		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOME RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1533	1hh8	A	10	140	7e-12	0.04	-0.12		NEUTROPHIL CYTOSOL FACTOR 2; CHAIN: A;	PHAGOCYTE OXIDASE FACTOR P67PHOX, NCF-2; PHAGOCYTE OXIDASE FACTOR, SH3 DOMAIN, REPEAT, TPR REPEAT
1533	1hxi	A	451	539	2.8e-08	0.20	-0.11		PEROXISOME TARGETING SIGNAL 1 RECEPTOR PEX5; CHAIN: A;	TRANSPORT PROTEIN PEX5; ALPHA HELICAL
1533	1ihg	A	409	538	9.8e-14	0.29	-0.08		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRATRICOPEPTIDE
1533	1ihg	A	444	519	7.2e-07	0.04	0.63		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRATRICOPEPTIDE

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1533	1lhg	A	449	572	1.4e-12	0.15	-0.14		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRA TRICOPEPTIDE
1533	1lhg	A	483	586	5.6e-11	0.17	-0.19		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRA TRICOPEPTIDE
1534	1b07	A	635	667	0.0084	-0.19	0.03		PROTO-ONCOGENE CRK (CRK); CHAIN: A; HIS TAG; CHAIN: B; SH3 PEPTOID INHIBITOR; CHAIN: C;	SH3 DOMAIN P38, ADAPTER MOLECULE CRK; SH3 DOMAIN, INHIBITORS, PEPTOIDS, PROTEIN-PROTEIN 2 RECOGNITION, PROLINE-RICH MOTIFS, SIGNAL TRANSDUCTION
1534	1b0x	A	692	753	3.6e-12	0.84	1.00		EPH4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
1534	1gbr	A	635	674	0.00024	-0.01	0.06		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL IGBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE IGBR 4 (NMR, 29 STRUCTURES) IGBR 5	
1534	1gcq	B	635	670	2.4e-06	0.13	0.00		GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; CHAIN: A; B; VAV PROTO-ONCOGENE; CHAIN: C;	SIGNALING PROTEIN/SIGNALING PROTEIN SH3 DOMAIN, PROTEIN-PROTEIN COMPLEX, GRB2, VAV

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1534	1hsq		635	675	0.00096	-0.39	0.10		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
1534	1pwt		635	670	0.00024	-0.05	0.07		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1534	1sem	A	635	667	7.2e-06	-0.15	0.07		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
1534	1sge		692	753	1.2e-11	0.53	0.94		EPHRIN TYPE-B RECEPTOR 2; CHAIN: NULL;	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2 PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1534	1tuc		635	676	3.6e-06	-0.55	0.13		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
1538	1a06		1	270	1.1e-72			108.10	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1538	1apm	E	1	270	7e-66			70.09	TRANSFERASE(PHOSPHOTRANSFERASE) \$C- /AMP\$-DEPENDENT PROTEIN KINASE	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1538	1bi8	A	10	243	1.4e-34			62.31	(E.C.2.7.1.37) (\$C/APK\$) IAPM 3 (CATALYTIC SUBUNIT) "ALPHA" ISOENZYME MUTANT WITH SER 139 IAPM 4 REPLACED BY ALA (/S139AS) COMPLEX WITH THE PEPTIDE IAPM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 IAPM 6	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1538	1blx	A	1	251	4.2e-37			58.85	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1538	1cm8	A	1	270	7e-41			64.67	PHOSPHORYLATED MAP KINASE P38-GAMMA; CHAIN: A, B;	TRANSFERASE STRESS-ACTIVATED PROTEIN KINASE-3, ERK6, ERK5; P38-GAMMA, GAMMA, PHOSPHORYLATION, MAP KINASE
1538	1cmk	E	1	270	7e-67			65.16	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1538	1cjp	E	1	270	2.8e-67			74.46	CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
									TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
1538	1elx	A	1	257	1.1e-45			75.76	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: A;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, CELL DIVISION, 2 MITOSIS, INHIBITION
1538	1f3m	C	2	262	9.8e-45			75.17	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1538	1fgk	A	1	244	4.2e-21			50.75	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1538	1ftc	A	1	270	1.4e-63			87.56	CAMP-DEPENDENT PROTEIN KINASE TYPE 1; CHAIN: A;	TRANSFERASE TPK1 DELTA; CAMP-DEPENDENT PROTEIN KINASE, OPEN CONFORMATION, PROTEIN 2 KINASE
1538	1hel		1	257	2.8e-46			66.51	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2, TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1538	1how	A	1	270	8.4e-29			57.03	SERINE/THREONINE-PROTEIN KINASE YMR216G; CHAIN: A;	CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1538	1ia8	A	1	253	4.2e-45			82.74	CHK1 CHECKPOINT KINASE; CHAIN: A;	TRANSFERASE PROTEIN KINASE
1538	1iep	A	1	253	2.8e-23			60.07	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1538	1kob	A	1	267	7e-65			75.19	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1538	1p38		1	270	1.4e-40			53.04	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1538	1phk		1	173	1.4e-59			55.11	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1538	1phk		1	246	9.8e-66			107.34	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1538	1pme		1	270	1.4e-40			81.42	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1538	1qpc	A	1	244	1.3e-21			57.16	LCK KINASE; CHAIN: A;	KINASE, TRANSFERASE
1538	1tki	A	5	269	9.8e-57			79.61	TTIN; CHAIN: A, B;	TRANSFERASE ALPHA BETA FOLD
1538	3erk		1	266	1.4e-40			70.45	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2, TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1540	1alh	A	725	752	0.0024	-0.24	0.86		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1540	1sp2		725	752	0.00024	0.25	0.71		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1540	1tf6	A	725	764	0.006	0.14	0.17		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2
1540	1ubd	C	725	752	0.0084	-0.07	0.96		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1540	2gli	A	725	752	0.0084	0.19	0.59		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	REGULATION/DNA COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1542	lapo		911	952	2.4e-15	0.41	0.75		COAGULATION FACTOR EGF-LIKE MODULE OF BLOOD COAGULATION FACTOR X (N-TERMINAL, LAPO 3 APO FORM) (NMR, 13 STRUCTURES) LAPO 4	
1542	laut	L	915	1050	1.2e-19	0.12	-0.05		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1542	lbff		913	948	2.4e-15	0.58	1.00		FACTOR VII; CHAIN: NULL;	BLOOD COAGULATION BLOOD COAGULATION, EGF, HYDROLASE, SERINE PROTEASE
1542	lbk9		913	1050	8.4e-27	0.16	-0.17		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE HYDROLASE, PHOSPHOLIPASE A2, PLATELET AGGREGATION INHIBITOR, 2 PBPB HEADER MODRES
1542	ldan	L	1018	1108	4.8e-18	0.19	0.03		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1542	1dan	L	913	1057	1.1e-22	0.18	0.53		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFPRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1542	1dqb	A	913	1049	1.2e-15	0.13	-0.18		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1542	1dqb	A	998	1095	3.6e-17	0.58	0.09		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1542	1dva	L	913	1057	6e-23	0.13	0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPND)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
1542	1dx5	I	913	1044	3.6e-26	0.21	0.15		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1542	1edn	B	913	948	9.6e-14	0.94	1.00		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE,

Table 5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1542	legf		913	950	2.4e-13	0.85	0.95		GROWTH FACTOR EPIDERMAL GROWTH FACTOR (EGF) (NMR, 16 STRUCTURES) 1EGF 3	EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
1542	lemn		998	1066	4.8e-19	0.16	0.84		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1542	legg	A	913	1099	8.4e-25	0.06	-0.13		PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A, B;	OXIDOREDUCTASE COX-1; EGF DOMAIN, NSAIID BINDING, IBUPROFEN, MEMBRANE-BINDING 2 DOMAIN, CYCLOOXYGENASE, PEROXIDASE, OXIDOREDUCTASE, 3
1542	lext	A	920	1108	1.2e-26	0.37	0.24		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	DIOXYGENASE, PEROXIDASE SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1542	lfe	A	913	949	7.2e-14	1.02	1.00		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
1542	lfak	L	913	1057	6e-23	0.19	0.59		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1542	1fak	L	998	1099	1.2e-16	-0.00	0.01		BLOOD COAGULATION FACTOR VIIA; CHAIN: I; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1542	1fsb		916	952	2.4e-15	0.83	0.87		P-SELECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN EGF-LIKE DOMAIN, CELL ADHESION PROTEIN, TRANSMEMBRANE, 2 GLYCOPROTEIN
1542	1g44	B	910	1057	3.6e-16	-0.00	-0.18		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1542	1hj7	A	1002	1080	2.4e-19	0.34	0.70		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1542	1hj7	A	915	1045	4.8e-20	0.24	0.10		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1542	1igr	A	913	1082	3.6e-18	0.03	-0.17		INSULIN-LIKE GROWTH FACTOR RECEPTOR I;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR